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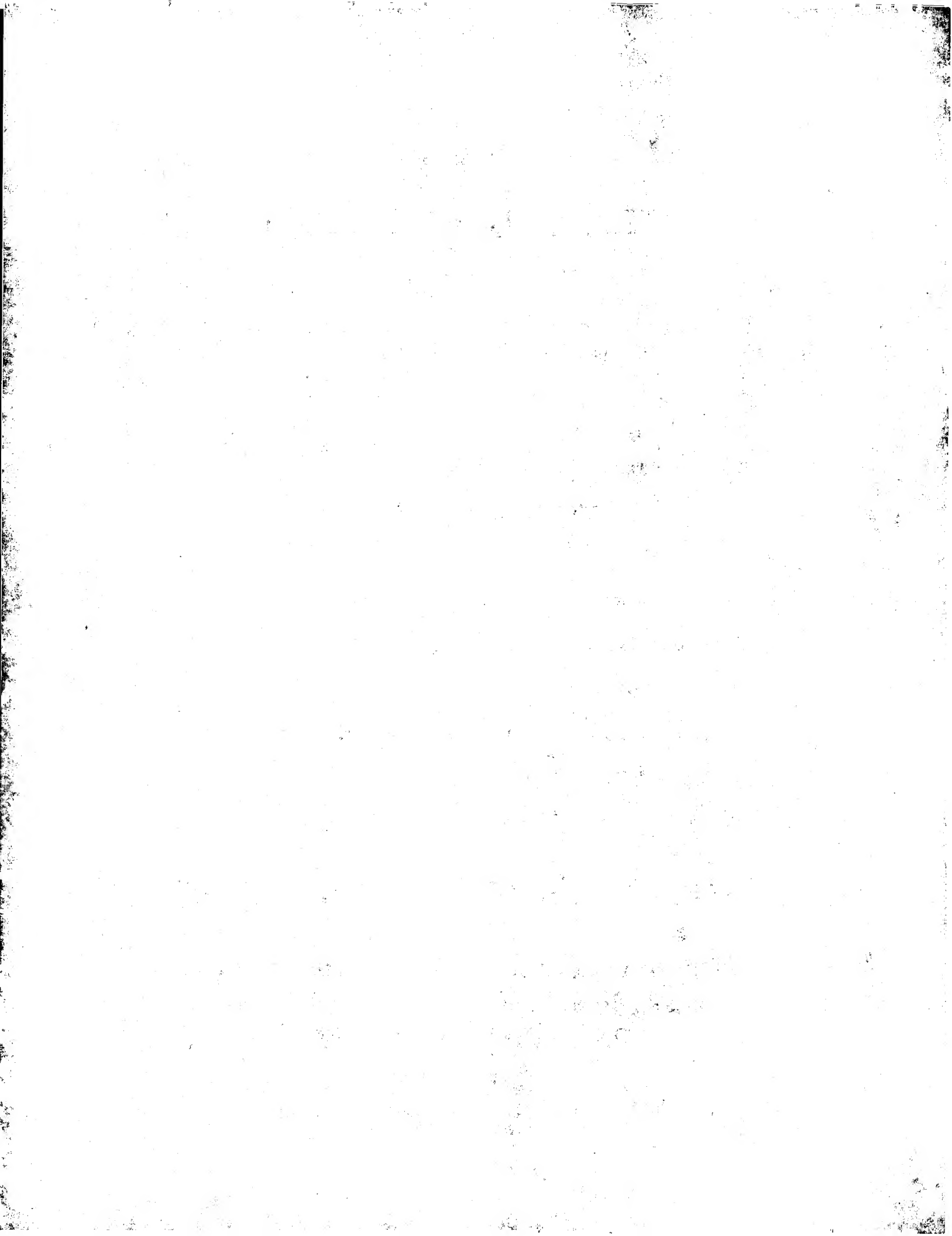
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(54) Title: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION			
(57) Abstract  The present invention relates to peptides which exhibit potent anti-retroviral activity. The peptides of the invention comprise DP178 (SEQ ID:1) peptide corresponding to amino acids 638 to 673 of the HIV-1 <sub>LAI</sub> gp41 protein, and fragments, analogs and homologs of DP178. The invention further relates to the uses of such peptides as inhibitory of human and non-human retroviral, especially HIV, transmission to uninfected cells.			



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**METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION**

This is a Continuation-In-Part of Serial No. 08/360,107 filed December 20, 1994, which is a  
5 Continuation-In-Part of Serial No. 08/255,208 filed June 7, 1994, which is a Continuation-In-Part of Serial No. 08/073,028 filed June 7, 1993, each of which is incorporated herein by reference in its entirety. This invention was made with Government  
10 support under Grant No. AI-30411-02 awarded by the National Institutes of Health. The Government has certain rights in the invention.

**1. INTRODUCTION**

15 The present invention relates, first, to DP178 (SEQ ID NO:1), a peptide corresponding to amino acids 638 to 673 of the HIV-1<sub>LAI</sub> transmembrane protein (TM) gp41, and portions or analogs of DP178 (SEQ ID NO:1), which exhibit anti-membrane fusion capability,  
20 antiviral activity, such as the ability to inhibit HIV transmission to uninfected CD-4<sup>+</sup> cells, or an ability to modulate intracellular processes involving coiled-coil peptide structures. Further, the invention relates to the use of DP178 (SEQ ID NO:1) and DP178  
25 portions and/or analogs as antifusogenic or antiviral compounds or as inhibitors of intracellular events involving coiled-coil peptide structures. The present invention also relates to peptides analogous to DP107 (SEQ ID NO:25), a peptide corresponding to amino acids  
30 558 to 595 of the HIV-1<sub>LAI</sub> transmembrane protein (TM) gp41, having amino acid sequences present in other viruses, such as enveloped viruses, and/or other organisms, and further relates to the uses of such peptides. These peptides exhibit anti-membrane fusion  
35 capability, antiviral activity, or the ability to



modulate intracellular processes involving coiled-coil peptide structures. The present invention additionally relates to methods for identifying compounds that disrupt the interaction between DP178 and DP107, and/or between DP107-like and DP178-like peptides. Further, the invention relates to the use of the peptides of the invention as diagnostic agents. For example, a DP178 peptide may be used as an HIV subtype-specific diagnostic. The invention is demonstrated, first, by way of an Example wherein DP178 (SEQ ID:1), and a peptide whose sequence is homologous to DP178 are each shown to be potent, non-cytotoxic inhibitors of HIV-1 transfer to uninfected CD-4<sup>+</sup> cells. The invention is further demonstrated by Examples wherein peptides having structural and/or amino acid motif similarity to DP107 and DP178 are identified in a variety of viral and nonviral organisms, and in examples wherein a number of such identified peptides derived from several different viral systems are demonstrated to exhibit antiviral activity.

## 2. BACKGROUND OF THE INVENTION

### 2.1 MEMBRANE FUSION EVENTS

Membrane fusion is a ubiquitous cell biological process (for a review, see White, J.M., 1992, Science 258:917-924). Fusion events which mediate cellular housekeeping functions, such as endocytosis, constitutive secretion, and recycling of membrane components, occur continuously in all eukaryotic cells.

Additional fusion events occur in specialized cells. Intracellularly, for example, fusion events are involved in such processes as occur in regulated exocytosis of hormones, enzymes and neurotransmitters.



Intercellularly, such fusion events feature prominently in, for example, sperm-egg fusion and myoblast fusion.

5 Fusion events are also associated with disease states. For example, fusion events are involved in the formation of giant cells during inflammatory reactions, the entry of all enveloped viruses into cells, and, in the case of human immunodeficiency virus (HIV), for example, are responsible for the virally induced cell-cell fusion which leads to cell  
10 death.

## 2.2. THE HUMAN IMMUNODEFICIENCY VIRUS

The human immunodeficiency virus (HIV) has been implicated as the primary cause of the slowly  
15 degenerative immune system disease termed acquired immune deficiency syndrome (AIDS) (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo, R. et al., 1984, Science 224:500-503). There are at least two distinct types of HIV: HIV-1 (Barre-Sinoussi, F. et al.,  
20 et al., 1983, Science 220:868-870; Gallo R. et al., 1984, Science 224:500-503) and HIV-2 (Clavel, F. et al., 1986, Science 233:343-346; Guyader, M. et al., 1987, Nature 326:662-669). Further, a large amount of genetic heterogeneity exists within populations of  
25 each of these types. Infection of human CD-4<sup>+</sup> T-lymphocytes with an HIV virus leads to depletion of the cell type and eventually to opportunistic infections, neurological dysfunctions, neoplastic growth, and ultimately death.

30 HIV is a member of the lentivirus family of retroviruses (Teich, N. et al., 1984, RNA Tumor Viruses, Weiss, R. et al., eds., CSH-Press, pp. 949-956). Retroviruses are small enveloped viruses that contain a diploid, single-stranded RNA genome, and  
35



replicate via a DNA intermediate produced by a virally-encoded reverse transcriptase, an RNA-dependent DNA polymerase (Varmus, H., 1988, *Science* 240:1427-1439). Other retroviruses include, for example, oncogenic viruses such as human T-cell  
5 leukemia viruses (HTLV-I, -II, -III), and feline leukemia virus.

The HIV viral particle consists of a viral core, composed of capsid proteins, that contains the viral RNA genome and those enzymes required for early  
10 replicative events. Myristylated Gag protein forms an outer viral shell around the viral core, which is, in turn, surrounded by a lipid membrane enveloped derived from the infected cell membrane. The HIV enveloped surface glycoproteins are synthesized as a single 160  
15 Kd precursor protein which is cleaved by a cellular protease during viral budding into two glycoproteins, gp41 and gp120. gp41 is a transmembrane protein and gp120 is an extracellular protein which remains non-covalently associated with gp41, possibly in a  
20 trimeric or multimeric form (Hammarskjold, M. and Rekosh, D., 1989, *Biochem. Biophys. Acta* 989:269-280).

HIV is targeted to CD-4<sup>+</sup> cells because the CD-4 cell surface protein acts as the cellular receptor for the HIV-1 virus (Dalglish, A. *et al.*, 1984, *Nature*  
25 312:763-767; Klatzmann *et al.*, 1984, *Nature* 312:767-768; Maddon *et al.*, 1986, *Cell* 47:333-348). Viral entry into cells is dependent upon gp120 binding the cellular CD-4<sup>+</sup> receptor molecules (McDougal, J.S. *et al.*, 1986, *Science* 231:382-385; Maddon, P.J. *et al.*,  
30 1986, *Cell* 47:333-348) and thus explains HIV's tropism for CD-4<sup>+</sup> cells, while gp41 anchors the enveloped glycoprotein complex in the viral membrane.

35



### 2.3. HIV TREATMENT

HIV infection is pandemic and HIV associated diseases represent a major world health problem. Although considerable effort is being put into the  
5 successful design of effective therapeutics, currently no curative anti-retroviral drugs against AIDS exist. In attempts to develop such drugs, several stages of the HIV life cycle have been considered as targets for therapeutic intervention (Mitsuya, H. et al., 1991,  
10 FASEB J. 5:2369-2381). For example, virally encoded reverse transcriptase has been one focus of drug development. A number of reverse-transcriptase-targeted drugs, including 2',3'-dideoxynucleoside analogs such as AZT, ddI, ddC, and d4T have been  
15 developed which have been shown to be active against HIV (Mitsuya, H. et al., 1991, Science 249:1533-1544). While beneficial, these nucleoside analogs are not curative, probably due to the rapid appearance of drug resistant HIV mutants (Lander, B. et al., 1989,  
20 Science 243:1731-1734). In addition, the drugs often exhibit toxic side effects such as bone marrow suppression, vomiting, and liver function abnormalities.

Attempts are also being made to develop drugs  
25 which can inhibit viral entry into the cell, the earliest stage of HIV infection. Here, the focus has thus far been on CD4, the cell surface receptor for HIV. Recombinant soluble CD4, for example, has been shown to inhibit infection of CD-4<sup>+</sup> T-cells by some  
30 HIV-1 strains (Smith, D.H. et al., 1987, Science 238:1704-1707). Certain primary HIV-1 isolates, however, are relatively less sensitive to inhibition by recombinant CD-4 (Daar, E. et al., 1990, Proc. Natl. Acad. Sci. USA 87:6574-6579). In addition,  
35



recombinant soluble CD-4 clinical trials have produced inconclusive results (Schooley, R. et al., 1990, Ann. Int. Med. 112:247-253; Kahn, J.O. et al., 1990, Ann. Int. Med. 112:254-261; Yarchoan, R. et al., 1989, Proc. Vth Int. Conf. on AIDS, p. 564, MCP 137).

5       The late stages of HIV replication, which involve crucial virus-specific secondary processing of certain viral proteins, have also been suggested as possible anti-HIV drug targets. Late stage processing is dependent on the activity of a viral protease, and  
10       drugs are being developed which inhibit this protease (Erickson, J., 1990, Science 249:527-533). The clinical outcome of these candidate drugs is still in question.

15       Attention is also being given to the development of vaccines for the treatment of HIV infection. The HIV-1 enveloped proteins (gp160, gp120, gp41) have been shown to be the major antigens for anti-HIV antibodies present in AIDS patients (Barin, et al., 1985, Science 228:1094-1096). Thus far, therefore,  
20       these proteins seem to be the most promising candidates to act as antigens for anti-HIV vaccine development. To this end, several groups have begun to use various portions of gp160, gp120, and/or gp41 as immunogenic targets for the host immune system.  
25       See for example, Ivanoff, L. et al., U.S. Pat. No. 5,141,867; Saith, G. et al., WO 92/22,654; Shafferman, A., WO 91/09,872; Formoso, C. et al., WO 90/07,119. Clinical results concerning these candidate vaccines, however, still remain far in the future.

30       Thus, although a great deal of effort is being directed to the design and testing of anti-retroviral drugs, a truly effective, non-toxic treatment is still needed.

35



### 3. SUMMARY OF THE INVENTION

The present invention relates, first, to DP178 (SEQ ID:1), a 36-amino acid synthetic peptide corresponding to amino acids 638 to 673 of the transmembrane protein (TM) gp41 from the HIV-1 isolate LAI (HIV-1<sub>LAI</sub>), which exhibits potent anti-HIV-1 activity. As evidenced by the Example presented below, in Section 6, the DP178 (SEQ ID:1) antiviral activity is so high that, on a weight basis, no other known anti-HIV agent is effective at concentrations as low as those at which DP178 (SEQ ID:1) exhibits its inhibitory effects.

The invention further relates to those portions and analogs of DP178 which also show such antiviral activity, and/or show anti-membrane fusion capability, or an ability to modulate intracellular processes involving coiled-coil peptide structures. The term "DP178 analog" refers to a peptide which contains an amino acid sequence corresponding to the DP178 peptide sequence present within the gp41 protein of HIV-1<sub>LAI</sub>, but found in viruses and/or organisms other than HIV-1<sub>LAI</sub>. Such DP178 analog peptides may, therefore, correspond to DP178-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1<sub>LAI</sub>, as well as non-enveloped viruses. Further, such analogous DP178 peptides may also correspond to DP178-like amino acid sequences present in nonviral organisms.

The invention further relates to peptides DP107 (SEQ ID NO:25) analogs. DP107 is a peptide corresponding to amino acids 558-595 of the HIV-1<sub>LAI</sub> transmembrane protein (TM) gp41. The term "DP107 analog" as used herein refers to a peptide which contains an amino acid sequence corresponding to the



DP107 peptide sequence present within the gp41 protein of HIV-1<sub>LAI</sub>, but found in viruses and organisms other than HIV-1<sub>LAI</sub>. Such DP107 analog peptides may, therefore, correspond to DP107-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1<sub>LAI</sub>, as well as non-enveloped viruses. Further, such DP107 analog peptides may also correspond to DP107-like amino acid sequences present in nonviral organisms.

Further, the peptides of the invention include DP107 analog and DP178 analog peptides having amino acid sequences recognized or identified by the 107x178x4, ALLMOTI5 and/or PLZIP search motifs described herein.

The peptides of the invention may, for example, exhibit antifusogenic activity, antiviral activity, and/or may have the ability to modulate intracellular processes which involve coiled-coil peptide structures. With respect to the antiviral activity of the peptides of the invention, such an antiviral activity includes, but is not limited to the inhibition of HIV transmission to uninfected CD-4<sup>+</sup> cells. Additionally, the antifusogenic capability, antiviral activity or intracellular modulatory activity of the peptides of the invention merely requires the presence of the peptides of the invention, and, specifically, does not require the stimulation of a host immune response directed against such peptides.

The peptides of the invention may be used, for example, as inhibitors of membrane fusion-associated events, such as, for example, the inhibition of human and non-human retroviral, especially HIV, transmission to uninfected cells. It is further contemplated that



the peptides of the invention may be used as modulators of intracellular events involving coiled-coil peptide structures.

5 The peptides of the invention may, alternatively, be used to identify compounds which may themselves exhibit antifusogenic, antiviral, or intracellular modulatory activity. Additional uses include, for example, the use of the peptides of the invention as organism or viral type and/or subtype-specific diagnostic tools.

10 The terms "antifusogenic" and "anti-membrane fusion", as used herein, refer to an agent's ability to inhibit or reduce the level of membrane fusion events between two or more moieties relative to the level of membrane fusion which occurs between said  
15 moieties in the absence of the peptide. The moieties may be, for example, cell membranes or viral structures, such as viral envelopes or pili. The term "antiviral", as used herein, refers to the compound's ability to inhibit viral infection of cells, via, for  
20 example, cell-cell fusion or free virus infection. Such infection may involve membrane fusion, as occurs in the case of enveloped viruses, or some other fusion event involving a viral structure and a cellular structure (e.g., such as the fusion of a viral pilus  
25 and bacterial membrane during bacterial conjugation).

It is also contemplated that the peptides of the invention may exhibit the ability to modulate intracellular events involving coiled-coil peptide structures. "Modulate", as used herein, refers to a  
30 stimulatory or inhibitory effect on the intracellular process of interest relative to the level or activity of such a process in the absence of a peptide of the invention.

35



Embodiments of the invention are demonstrated below wherein an extremely low concentration of DP178 (SEQ ID:1), and very low concentrations of a DP178 homolog (SEQ ID:3) are shown to be potent inhibitors of HIV-1 mediated CD-4<sup>+</sup> cell-cell fusion (*i.e.*,  
5 syncytial formation) and infection of CD-4<sup>+</sup> cells by cell-free virus. Further, it is shown that DP178 (SEQ ID:1) is not toxic to cells, even at concentrations 3 logs higher than the inhibitory DP-178 (SEQ ID:1) concentration.

10 The present invention is based, in part, on the surprising discovery that the DP107 and DP178 domains of the HIV gp41 protein-non-covalently complex with each other, and that their interaction is required for the normal infectivity of the virus. This discovery  
15 is described in the Example presented, below, in Section 8. The invention, therefore, further relates to methods for identifying antifusogenic, including antiviral, compounds that disrupt the interaction between DP107 and DP178, and/or between DP107-like and  
20 DP178-like peptides.

Additional embodiments of the invention (specifically, the Examples presents in Sections 9-16 and 19-25, below) are demonstrated, below, wherein  
25 peptides, from a variety of viral and nonviral sources, having structural and/or amino acid motif similarity to DP107 and DP178 are identified, and search motifs for their identification are described. Further, Examples (in Sections 17, 18, 25-29) are presented wherein a number of the peptides of the  
30 invention are demonstrated exhibit substantial antiviral activity or activity predictive of antiviral activity.

35



### 3.1. DEFINITIONS

Peptides are defined herein as organic compounds comprising two or more amino acids covalently joined by peptide bonds. Peptides may be referred to with  
5 respect to the number of constituent amino acids, i.e., a dipeptide contains two amino acid residues, a tripeptide contains three, etc. Peptides containing ten or fewer amino acids may be referred to as oligopeptides, while those with more than ten amino  
10 acid residues are polypeptides. Such peptides may also include any of the modifications and additional amino and carboxy groups as are described herein.

Peptide sequences defined herein are represented by one-letter symbols for amino acid residues as  
15 follows:

A (alanine)  
R (arginine)  
N (asparagine)  
D (aspartic acid)  
C (cysteine)  
20 Q (glutamine)  
E (glutamic acid)  
G (glycine)  
H (histidine)  
I (isoleucine)  
L (leucine)  
K (lysine)  
M (methionine)  
25 F (phenylalanine)  
P (proline)  
S (serine)  
T (threonine)  
W (tryptophan)  
Y (tyrosine)  
V (valine)

30

35



#### 4. BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. Amino acid sequence of DP178 (SEQ ID:1) derived from HIV<sub>LAI</sub>; DP178 homologs derived from HIV-1<sub>SP2</sub> (DP-185; SEQ ID:3), HIV-1<sub>RF</sub> (SEQ ID:4), and HIV-1<sub>MN</sub> (SEQ ID:5); DP178 homologs derived from amino acid sequences of two prototypic HIV-2 isolates, namely, HIV-2<sub>red</sub> (SEQ ID:6) and HIV-2<sub>NBZ</sub> (SEQ ID:7); control peptides: DP-180 (SEQ ID:2), a peptide incorporating the amino acid residues of DP178 in a scrambled sequence; DP-118 (SEQ ID:10) unrelated to DP178, which inhibits HIV-1 cell free virus infection; DP-125 (SEQ ID:8), unrelated to DP178, also inhibits HIV-1 cell free virus infection; DP-116 (SEQ ID:9), unrelated to DP178, is negative for inhibition of HIV-1 infection when tested using a cell-free virus infection assay. Throughout the figures, the one letter amino acid code is used.

FIG. 2. Inhibition of HIV-1 cell-free virus infection by synthetic peptides. IC<sub>50</sub> refers to the concentration of peptide that inhibits RT production from infected cells by 50% compared to the untreated control. Control: the level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 3. Inhibition of HIV-1 and HIV-2 cell-free virus infection by the synthetic peptide DP178 (SEQ ID:1). IC<sub>50</sub>: concentration of peptide that inhibits RT production by 50% compared to the untreated control. Control: Level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 4A-4B. Fusion Inhibition Assays. FIG 4A: DP178 (SEQ ID:1) inhibition of HIV-1 prototypic isolate-mediated syncytial formation; data represents the number of virus-induced syncytial per cell. FIG.



4B: DP-180 (SEQ ID:2) represents a scrambled control peptide; DP-185 (SEQ ID:3) represents a DP178 homolog derived from HIV-1<sub>SP2</sub> isolate; Control, refers to the number of syncytial produced in the absence of peptide.

5       FIG. 5. Fusion inhibition assay: HIV-1 vs. HIV-2. Data represents the number of virus-induced syncytial per well. ND: not done.

10       FIG. 6. Cytotoxicity study of DP178 (SEQ ID:1) and DP-116 (SEQ ID:9) on CEM cells. Cell proliferation data is shown.

15       FIG. 7. Schematic representation of HIV-gp41 and maltose binding protein (MBP)-gp41 fusion proteins. DP107 and DP178 are synthetic peptides based on the two putative helices of gp41. The letter P in the DP107 boxes denotes an Ile to Pro mutation at amino acid number 578. Amino acid residues are numbered according to Meyers et al., "Human Retroviruses and AIDS", 1991, Theoret. Biol. and Biophys. Group, Los Alamos Natl. Lab., Los Alamos, NM.

20       The proteins are more fully described, below, in Section 8.1.1.

FIG. 8. A point mutation alters the conformation and anti-HIV activity of M41.

25       FIG. 9. Abrogation of DP178 anti-HIV activity. Cell fusion assays were carried out in the presence of 10 nM DP178 and various concentrations of M41Δ178 or M41PA178.

30       FIG. 10. Binding of DP178 to leucine zipper of gp41 analyzed by FAb-D ELISA.

35       FIG. 11A-B. Models for a structural transition in the HIV-1 TM protein. Two models are proposed which indicate a structural transition from a native oligomer to a fusogenic state following a trigger event (possibly gp120 binding to CD4). Common



features of both models include (1) the native state is held together by noncovalent protein-protein interactions to form the heterodimer of gp120/41 and other interactions, principally through gp41 interactive sites, to form homo-oligomers on the virus surface of the gp120/41 complexes; (2) shielding of the hydrophobic fusogenic peptide at the N-terminus (F) in the native state; and (3) the leucine zipper domain (DP107) exists as a homo-oligomer coiled coil only in the fusogenic state. The major differences in the two models include the structural state (native or fusogenic) in which the DP107 and DP178 domains are complexed to each other. In the first model (FIG. 11A) this interaction occurs in the native state and in the second (FIG. 11B), it occurs during the fusogenic state. When triggered, the fusion complex in the model depicted in (A) is generated through formation of coiled-coil interactions in homologous DP107 domains resulting in an extended  $\alpha$ -helix. This conformational change positions the fusion peptide for interaction with the cell membrane. In the second model (FIG. 11B), the fusogenic complex is stabilized by the association of the DP178 domain with the DP107 coiled-coil.

FIG. 12. Motif design using heptad repeat positioning of amino acids of known coiled-coils.

FIG. 13. Motif design using proposed heptad repeat positioning of amino acids of DP107 and DP178.

FIG. 14. Hybrid motif design crossing GCN4 and DP107.

FIG. 15. Hybrid motif design crossing GCN4 and DP178.

FIG. 16. Hybrid motif design 107x178x4, crossing DP107 and DP178. This motif was found to be



the most consistent at identifying relevant DP107-like and DP178-like peptide regions.

FIG. 17. Hybrid motif design crossing GCN4, DP107, and DP178.

5 FIG. 18. Hybrid motif design ALLMOTI5 crossing GCN4, DP107, DP178, c-Fos c-Jun, c-Myc, and Flu Loop 36.

FIG. 19. PLZIP motifs designed to identify N-terminal proline-leucine zipper motifs.

10 FIG. 20. Search results for HIV-1 (BRU isolate) enveloped protein gp41. Sequence search motif designations: Spades (♠): 107x178x4; Hearts (♥) ALLMOTI5; Clubs (♣): PLZIR; Diamonds (♦): transmembrane region (the putative transmembrane domains were identified using a PC/Gene program  
15 designed to search for such peptide regions). Asterisk (\*): Lupas method. The amino acid sequences identified by each motif are bracketed by the respective characters. Representative sequences chosen based on 107x178x4 searches are underlined and  
20 in bold. DP107 and DP178 sequences are marked, and additionally double-underlined and italicized.

FIG. 21. Search results for human respiratory syncytial virus (RSV) strain A2 fusion glycoprotein F1. Sequence search motif designations  
25 are as in FIG. 20.

FIG. 22. Search results for simian immunodeficiency virus (SIV) enveloped protein gp41 (AGM3 isolate). Sequence search motif designations  
30 are as in FIG. 20.

FIG. 23. Search results for canine distemper virus (strain Onderstepoort) fusion glycoprotein 1. Sequence search motif designations  
are as in FIG. 20.

35



FIG. 24. Search results for newcastle disease virus (strain Australia-Victoria/32) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

5 FIG. 25. Search results for human parainfluenza 3 virus (strain NIH 47885) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

10 FIG. 26. Search results for influenza A virus (strain A/AICHI/2/68) hemagglutinin precursor HA2. Sequence search designations are as in FIG. 20.

FIG. 27A-D. Respiratory Syncytial Virus (RSV) peptide antiviral and circular dichroism data. FIG. 27A-B: Peptides derived from the F2 DP178/DP107-like region. Antiviral and CD data. FIG. 27C-D: 15 Peptides derived from the F1 DP107-like region. Peptide and CD data.

Antiviral activity (AV) is represented by the following qualitative symbols:

20 "- ", negative antiviral activity;  
"+/- ", antiviral activity at greater than 100 $\mu$ g/ml;  
"+ ", antiviral activity at between 50-100 $\mu$ g/ml;  
"++ ", antiviral activity at between 20-50 $\mu$ g/ml;  
25 "+++ ", antiviral activity at between 1-20 $\mu$ g/ml;  
"++++ ", antiviral activity at <1 $\mu$ g/ml.

CD data, referring to the level of helicity is represented by the following qualitative symbol:

30 "- ", no helicity;  
"+ ", 25-50% helicity;  
"++ ", 50-75% helicity;  
"+++ " 75-100% helicity.

IC<sub>50</sub> refers to the concentration of peptide necessary to produce only 50% of the number of syncytial relative to infected control cultures 35



containing no peptide.  $IC_{50}$  values were obtained using purified peptides only.

FIG. 28A-B. Respiratory Syncytial Virus (RSV) DP178-like region (F1) peptide antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as  
5 in FIG. 27A-D.  $IC_{50}$  values were obtained using purified peptides only.

FIG. 29A-B. Peptides derived from the HPIV3 F1 DP107-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG.  
10 27A-D. Purified peptides were used to obtain  $IC_{50}$  values, except where the values are marked by an asterisk (\*), in which cases, the  $IC_{50}$  values were obtained using a crude peptide preparation.

FIG. 30A-B. Peptides derived from the HPIV3 F1 DP178-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG.  
15 27A-D. Purified peptides were used to obtain  $IC_{50}$  values, except where the values are marked by an asterisk (\*), in which cases, the  $IC_{50}$  values were  
20 obtained using a crude peptide preparation.

FIG. 31. Motif search results for simian immunodeficiency virus (SIV) isolate MM251, enveloped polyprotein gp41. Sequence search designations are as  
25 in FIG. 20.

FIG. 32. Motif search results for Epstein-Barr Virus (Strain B95-8), glycoprotein gp110 precursor (designated gp115). BALF4. Sequence search designations are as in FIG. 20.

FIG. 33. Motif search results for Epstein-Barr Virus (Strain B95-8), BZLF1 trans-activator protein (designated EB1 or Zebra). Sequence search designations are as in FIG. 20. Additionally, "e" refers to a well known DNA binding domain and "+" refers to a well known dimerization domain, as defined  
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by Flemington and Speck (Flemington, E. and Speck, S.H., 1990, Proc. Natl. Acad. Sci. USA 87:9459-9463).

FIG. 34. Motif search results for measles virus (strain Edmonston), fusion glycoprotein F1. Sequence search designations are as in FIG. 20.

5 FIG. 35. Motif search results for Hepatitis B Virus (Subtype AYW), major surface antigen precursor S. Sequence search designations are as in FIG. 20.

FIG. 36. Motif search results for simian Mason-Pfizer monkey virus, enveloped (TM) protein gp20. Sequence search designations are as in FIG. 20.

10 FIG. 37. Motif search results for Pseudomonas aeruginosa, fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 38. Motif search results for Neisseria gonorrhoeae fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 39. Motif search results for Hemophilus influenzae fimbrial protein. Sequence search designations are as in FIG. 20.

20 FIG. 40. Motif search results for Staphylococcus aureus, toxic shock syndrome toxin-1. Sequence search designations are as in FIG. 20.

FIG. 41. Motif search results for Staphylococcus aureus enterotoxin Type E. Sequence search designations are as in FIG. 20.

25 FIG. 42. Motif search results for Staphylococcus aureus enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 43. Motif search results for Escherichia coli, heat labile enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 44. Motif search results for human c-fos proto-oncoprotein. Sequence search designations are as in FIG. 20.

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FIG. 45. Motif search results for human lupus KU autoantigen protein P70. Sequence search designations are as in FIG. 20.

5 FIG. 46. Motif search results for human zinc finger protein 10. Sequence search designations are as in FIG. 20.

FIG. 47. Measles virus (MeV) fusion protein DP178-like region antiviral and CD data. Antiviral symbols, CD symbols, and  $IC_{50}$  are as in FIG. 27A-D.  $IC_{50}$  values were obtained using purified peptides.

10 FIG. 48. Simian immunodeficiency virus (SIV) TM (fusion) protein DP178-like region antiviral data. Antiviral symbols are as in FIG. 27A-D "NT", not tested.

15 FIG. 49A-C. DP178-derived peptide antiviral data. The peptides listed herein were derived from the region surrounding the HIV-1 BRU isolate DP178 region (e.g., gp41 amino acid residues 615-717).

In instances where peptides contained DP178 point mutations, the mutated amino acid residues are shown with a shaded background. In instances in which the test peptide has had an amino and/or carboxy-terminal group added or removed (apart from the standard amido- and acetyl- blocking groups found on such peptides), such modifications are indicated. FIG. 49A: The column to the immediate right of the name of the test peptide indicates the size of the test peptide and points out whether the peptide is derived from a one amino acid peptide "walk" across the DP178 region. The next column to the right indicates whether the test peptide contains a point mutation, while the column to its right indicates whether certain amino acid residues have been added to or removed from the DP178-derived amino acid sequence. FIG 49B: The column to the immediate right of the test peptide name

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indicates whether the peptide represents a DP178 truncation, the next column to the right points out whether the peptide contains a point mutation, and the column to its right indicates whether the peptide contains amino acids which have been added to or removed from the DP178 sequence itself. FIG. 49C: The column to the immediate right of the test peptide name indicates whether the test peptide contains a point mutation, while the column to its right indicates whether amino acid residues have been added to or removed from the DP178 sequence itself.  $IC_{50}$  is as defined in FIG. 27A-D, and  $IC_{50}$  values were obtained using purified peptides except where marked with an asterisk (\*), in which case the  $IC_{50}$  was obtained using a crude peptide preparation.

FIG. 50. DP107 and DP107 gp41 region truncated peptide antiviral data.  $IC_{50}$  as defined in FIG. 27A-D, and  $IC_{50}$  values were obtained using purified peptides except where marked with an asterisk (\*), in which case the  $IC_{50}$  was obtained using a crude peptide preparation.

FIG. 51A-B. Epstein-Barr virus Strain B95-8 BZLF1 DP178/DP107 analog region peptide walks and electrophoretic mobility shift assay results. The peptides (T-423 to T-446, FIG. 51A; T-447 to T-461, FIG. 51B) represent one amino acid residue "walks" through the EBV Zebra protein region from amino acid residue 173 to 246.

The amino acid residue within this region which corresponds to the first amino acid residue of each peptide is listed to the left of each peptide, while the amino acid residue within this region which corresponds to the last amino acid residue of each peptide is listed to the right of each peptide. The



length of each test peptide is listed at the far right of each line, under the heading "Res".

"ACT" refers to a test peptide's ability to inhibit Zebra binding to its response element. "+" refers to a visible, but incomplete, abrogation of the response element/Zebra homodimer complex; "+++" refers to a complete abrogation of the complex; and "-" represents a lack of complex disruption.

FIG. 52A-B. Hepatitis B virus subtype AYW major surface antigen precursor S protein DP178/DP107 analog region and peptide walks. 52A depicts Domain I (S protein amino acid residues 174-220), which contains a potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain I. 52B depicts Domain II (S protein amino acid residues 233-291), which contains a second potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain II.

## 5. DETAILED DESCRIPTION OF THE INVENTION

Described herein are peptides which may exhibit antifusogenic activity, antiviral capability, and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. The peptides described include, first, DP178 (SEQ ID NO:1), a gp41-derived 36 amino acid peptide and fragments and analogs of DP178.

In addition, the peptides of the invention described herein include peptides which are DP107 analogs. DP107 (SEQ ID NO:25) is a 38 amino acid peptide corresponding to residues 558 to 595 of the HIV-1<sub>LAI</sub> transmembrane (TM) gp41 protein. Such DP107 analogs may exhibit antifusogenic capability, antiviral activity or an ability to modulate



intracellular processes involving coiled-coil structures.

Further, peptides of the invention include DP107 and DP178 are described herein having amino acid sequences recognized by the 107x178x4, ALLMOTI5, and  
5 PLZIP search motifs. Such motifs are also discussed.

Also described here are antifusogenic, antiviral, intracellular modulatory, and diagnostic uses of the peptides of the invention. Further, procedures are described for the use of the peptides of the invention  
10 for the identification of compounds exhibiting antifusogenic, antiviral or intracellular modulatory activity.

While not limited to any theory of operation, the following model is proposed to explain the potent  
15 anti-HIV activity of DP178, based, in part, on the experiments described in the Examples, *infra*. In the HIV protein, gp41, DP178 corresponds to a putative  $\alpha$ -helix region located in the C-terminal end of the gp41 ectodomain, and appears to associate with a distal  
20 site on gp41 whose interactive structure is influenced by the leucine zipper motif, a coiled-coil structure, referred to as DP107. The association of these two domains may reflect a molecular linkage or "molecular clasp" intimately involved in the fusion process. It  
25 is of interest that mutations in the C-terminal  $\alpha$ -helix motif of gp41 (*i.e.*, the D178 domain) tend to enhance the fusion ability of gp41, whereas mutations in the leucine zipper region (*i.e.*, the DP107 domain) decrease or abolish the fusion ability of the viral  
30 protein. It may be that the leucine zipper motif is involved in membrane fusion while the C-terminal  $\alpha$ -helix motif serves as a molecular safety to regulate the availability of the leucine zipper during virus-induced membrane fusion.

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On the basis of the foregoing, two models are proposed of gp41-mediated membrane fusion which are schematically shown in FIG. 11A-B. The reason for proposing two models is that the temporal nature of the interaction between the regions defined by DP107 and DP178 cannot, as yet, be pinpointed. Each model envisions two conformations for gp41 - one in a "native" state as it might be found on a resting virion. The other in a "fusogenic" state to reflect conformational changes triggered following binding of gp120 to CD4 and just prior to fusion with the target cell membrane. The strong binding affinity between gp120 and CD4 may actually represent the trigger for the fusion process obviating the need for a pH change such as occurs for viruses that fuse within intracellular vesicles. The two major features of both models are: (1) the leucine zipper sequences (DP107) in each chain of oligomeric enveloped are held apart in the native state and are only allowed access to one another in the fusogenic state so as to form the extremely stable coiled-coils, and (2) association of the DP178 and DP107 sites as they exist in gp41 occur either in the native or fusogenic state. FIG. 11A depicts DP178/DP107 interaction in the native state as a molecular clasp. On the other hand, if one assumes that the most stable form of the enveloped occurs in the fusogenic state, the model in FIG. 11B can be considered.

When synthesized as peptides, both DP107 and DP178 are potent inhibitors of HIV infection and fusion, probably by virtue of their ability to form complexes with viral gp41 and interfere with its fusogenic process; e.g., during the structural transition of the viral protein from the native structure to the fusogenic state, the DP178 and DP107



peptides may gain access to their respective binding sites on the viral gp41, and exert a disruptive influence. DP107 peptides which demonstrate anti-HIV activity are described in Applicants' co-pending application Serial No. 08/264,531, filed June 23, 1994, which is incorporated by reference herein in its entirety.

As shown in the Examples, infra, a truncated recombinant gp41 protein corresponding to the ectodomain of gp41 containing both DP107 and DP178 domains (excluding the fusion peptide, transmembrane region and cytoplasmic domain of gp41) did not inhibit HIV-1 induced fusion. However, when a single mutation was introduced to disrupt the coiled-coil structure of the DP107 domain -- a mutation which results in a total loss of biological activity of DP107 peptides -- the inactive recombinant protein was transformed to an active inhibitor of HIV-1 induced fusion. This transformation may result from liberation of the potent DP178 domain from a molecular clasp with the leucine zipper, DP107 domain.

For clarity of discussion, the invention will be described primarily for DP178 peptide inhibitors of HIV. However, the principles may be analogously applied to other viruses, both enveloped and nonenveloped, and to other non-viral organisms.

#### 5.1. DP178 AND DP178-LIKE PEPTIDES

The DP178 peptide (SEQ ID:1) of the invention corresponds to amino acid residues 638 to 673 of the transmembrane protein gp41 from the HIV-1<sub>LAI</sub> isolate, and has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH<sub>2</sub>-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:1)



In addition to the full-length DP178 (SEQ ID:1) 36-mer, the peptides of the invention may include truncations of the DP178 (SEQ ID:1) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. Truncations of DP178 (SEQ ID:1) peptides may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide), as shown in Tables I and IA, below.

Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group ( $-NH_2$ ) and "Z" may represent a carboxyl ( $-COOH$ ) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

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TABLE I  
DP178 (SEQ ID:1) CARBOXY TRUNCATIONS

X-YTS-Z  
 X-YTSL-Z  
 X-YTSLI-Z  
 X-YTSLIH-Z  
 5 X-YTSLIHS-Z  
 X-YTSLIHSL-Z  
 X-YTSLIHSLI-Z  
 X-YTSLIHSLIE-Z  
 X-YTSLIHSLIEE-Z  
 X-YTSLIHSLIEES-Z  
 X-YTSLIHSLIEESQ-Z  
 10 X-YTSLIHSLIEESQN-Z  
 X-YTSLIHSLIEESQNQ-Z  
 X-YTSLIHSLIEESQNQQ-Z  
 X-YTSLIHSLIEESQNQQE-Z  
 X-YTSLIHSLIEESQNQQEK-Z  
 X-YTSLIHSLIEESQNQQEKN-Z  
 X-YTSLIHSLIEESQNQQEKNE-Z  
 X-YTSLIHSLIEESQNQQEKNEQ-Z  
 15 X-YTSLIHSLIEESQNQQEKNEQE-Z  
 X-YTSLIHSLIEESQNQQEKNEQEL-Z  
 X-YTSLIHSLIEESQNQQEKNEQELL-Z  
 X-YTSLIHSLIEESQNQQEKNEQELLE-Z  
 X-YTSLIHSLIEESQNQQEKNEQELLELD-Z  
 X-YTSLIHSLIEESQNQQEKNEQELLELDK-Z  
 20 X-YTSLIHSLIEESQNQQEKNEQELLELDKW-Z  
 X-YTSLIHSLIEESQNQQEKNEQELLELDKWA-Z  
 X-YTSLIHSLIEESQNQQEKNEQELLELDKWas-Z  
 X-YTSLIHSLIEESQNQQEKNEQELLELDKWasLW-Z  
 X-YTSLIHSLIEESQNQQEKNEQELLELDKWasLWN-Z  
 X-YTSLIHSLIEESQNQQEKNEQELLELDKWasLWNW-Z  
 25 X-YTSLIHSLIEESQNQQEKNEQELLELDKWasLWNWF-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxy, dansyl, or  
 30 T-butyloxycarbonyl; an acetyl group; a 9-  
 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
 T-butyloxycarbonyl group; a macromolecular carrier  
 35 group including but not limited to lipid-fatty acid  
 conjugates, polyethylene glycol, or carbohydrates.



TABLE IA  
DP178 (SEQ ID:1) AMINO TRUNCATIONS

	X-NWF-Z
	X-WNWF-Z
	X-LWNWF-Z
	X-SLWNWF-Z
5	X-ASLWNWF-Z
	X-WASLWNWF-Z
	X-KWASLWNWF-Z
	X-DKWASLWNWF-Z
	X-LDKWASLWNWF-Z
	X-ELDKWASLWNWF-Z
	X-LELDKWASLWNWF-Z
10	X-LLELDKWASLWNWF-Z
	X-ELLELDKWASLWNWF-Z
	X-QELLELDKWASLWNWF-Z
	X-EQELLELDKWASLWNWF-Z
	X-NEQELLELDKWASLWNWF-Z
	X-KNEQELLELDKWASLWNWF-Z
	X-EKNEQELLELDKWASLWNWF-Z
	X-QEKNEQELLELDKWASLWNWF-Z
15	X-QQEKNEQELLELDKWASLWNWF-Z
	X-NQQEKNEQELLELDKWASLWNWF-Z
	X-QNQQEKNEQELLELDKWASLWNWF-Z
	X-SQNQQEKNEQELLELDKWASLWNWF-Z
	X-ESQNQQEKNEQELLELDKWASLWNWF-Z
	X-EESQNQQEKNEQELLELDKWASLWNWF-Z
	X-IEESQNQQEKNEQELLELDKWASLWNWF-Z
20	X-LIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-SLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-HSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-IHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-LIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-SLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-TSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
25	X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.



The peptides of the invention also include DP178-like peptides. "DP178-like", as used herein, refers, first, to DP178 and DP178 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-178-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP178. The DP178-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP178-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP178-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP178 peptides of the invention. Utilizing the DP178 and DP178 analog sequences described herein, the skilled artisan can readily compile DP178 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids of similar charge, size, and/or



hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The insertions may be made at the carboxy or amino terminal end of the DP178 or DP178 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP178 region of the gp41 protein.



Deletions of DP178 (SEQ ID:1) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP178 or DP178-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are further described, below, in Section 5.3.

## 5.2. DP107 AND DP107-LIKE PEPTIDES

Further, the peptides of the invention include peptides having amino acid sequences corresponding to DP107 analogs. DP107 is a 38 amino acid peptide which exhibits potent antiviral activity, and corresponds to residues 558 to 595 of HIV-1<sub>LAI</sub> transmembrane (TM) gp41 protein, as shown here:

NH<sub>2</sub>-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-COOH  
(SEQ ID:25)

In addition to the full-length DP107 (SEQ ID:25) 38-mer, the peptides of the invention may include truncations of the DP107 (SEQ ID:25) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes



involving coiled-coil peptide structures. Truncations of DP107 (SEQ ID:25) peptides may comprise peptides of between 3 and 38 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 38-mer polypeptide), as shown in Tables II and IIA, below.

5 Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group ( $-NH_2$ ) and "Z" may represent a carboxyl ( $-COOH$ ) group. Alternatively, "X" may represent a hydrophobic group, including but not  
10 limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or  
15 peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred  
20 "X" or "Z" macromolecular group is a peptide group.

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**TABLE II**  
**DP107 (SEQ ID:25) CARBOXY TRUNCATIONS**

X-NNL-Z  
 X-NNLL-Z  
 X-NNLLR-Z  
 5 X-NNLLRA-Z  
 X-NNLLRAI-Z  
 X-NNLLRAIE-Z  
 X-NNLLRAIEA-Z  
 X-NNLLRAIEAQ-Z  
 X-NNLLRAIEAQQ-Z  
 X-NNLLRAIEAQQH-Z  
 10 X-NNLLRAIEAQQHL-Z  
 X-NNLLRAIEAQQHLL-Z  
 X-NNLLRAIEAQQHLLQ-Z  
 X-NNLLRAIEAQQHLLQL-Z  
 X-NNLLRAIEAQQHLLQLT-Z  
 X-NNLLRAIEAQQHLLQLTV-Z  
 X-NNLLRAIEAQQHLLQLTVW-Z  
 X-NNLLRAIEAQQHLLQLTVWQ-Z  
 15 X-NNLLRAIEAQQHLLQLTVWQI-Z  
 X-NNLLRAIEAQQHLLQLTVWQIK-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQ-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQL-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQLQ-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQLQA-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQLQAR-Z  
 20 X-NNLLRAIEAQQHLLQLTVWQIKQLQARI-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQLQARIL-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILA-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAV-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVE-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVER-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERY-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYL-Z  
 25 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLK-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKD-Z  
 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-Z

The one letter amino acid code is used.

Additionally,

- 30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.  
 35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.



TABLE IIA  
DP178 (SEQ ID:25) AMINO TRUNCATIONS

	X-KDQ-	Z
	X-LKDQ-	Z
5	X-YLKDQ-	Z
	X-RYLKDQ-	Z
	X-ERYLKDQ-	Z
	X-VERYLKDQ-	Z
	X-AVERYLKDQ-	Z
	X-LAVERYLKDQ-	Z
	X-ILAVERYLKDQ-	Z
10	X-RILAVERYLKDQ-	Z
	X-ARILAVERYLKDQ-	Z
	X-QARILAVERYLKDQ-	Z
	X-LQARILAVERYLKDQ-	Z
	X-QLQARILAVERYLKDQ-	Z
	X-KQLQARILAVERYLKDQ-	Z
	X-IKQLQARILAVERYLKDQ-	Z
	X-QIKQLQARILAVERYLKDQ-	Z
15	X-WQIKQLQARILAVERYLKDQ-	Z
	X-VWQIKQLQARILAVERYLKDQ-	Z
	X-TVWQIKQLQARILAVERYLKDQ-	Z
	X-LTVWQIKQLQARILAVERYLKDQ-	Z
	X-QLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LLQLTVWQIKQLQARILAVERYLKDQ-	Z
20	X-HLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-QHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-QQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-AQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-EAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-IEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-AIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-RAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
25	X-LRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-NLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z

The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.



The peptides of the invention also include DP107-like peptides. "DP107-like", as used herein, refers, first, to DP107 and DP107 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-107-like" refers to  
5 peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP107. The DP107-like peptides of the invention may exhibit antifusogenic or antiviral  
10 activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP107-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability,  
15 or reduced host immune recognition.

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP107-corresponding regions of HIV-1 and HIV-2. The amino acid  
20 conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP107 peptides of  
25 the invention. Utilizing the DP107 and DP107 analog sequences described herein, the skilled artisan can readily compile DP107 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid  
30 substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence  
35 with amino acids of similar charge, size, and/or



hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids possessing  
5 dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The  
10 insertions may be made at the carboxy or amino terminal end of the DP107 or DP107 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that  
15 insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP107 (SEQ.ID:25) or DP107  
20 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to  
25 modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein  
30 regions either amino to or carboxy to the actual DP107 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP107  
35 region of the gp41 protein.



Deletions of DP107 (SEQ ID:25) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP107 or DP107-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP107 and DP107 truncations are more fully described in Applicants' co-pending U.S. Patent Application Ser. No. 08/374,666, filed January 27, 1995, and which is incorporated herein by reference in its entirety. DP107 analogs are further described, below, in Section 5.3.

### 5.3. DP107 and DP178 ANALOGS

Peptides corresponding to analogs of the DP178, DP178 truncations, DP107 and DP107 truncation sequences of the invention, described, above, in Sections 5.1 and 5.2 may be found in other viruses, including, for example, non-HIV-1<sub>LAI</sub> enveloped viruses, non-enveloped viruses and other non-viral organisms.

The term "analog", as used herein, refers to a peptide which is recognized or identified via the 107x178x4, ALLMOTI5 and/or PLZIP search strategies discussed below. Further, such peptides may exhibit antifusogenic capability, antiviral activity, or the



ability to modulate intracellular processes involving coiled-coil structures.

Such DP178 and DP107 analogs may, for example, correspond to peptide sequences present in TM proteins of enveloped viruses and may, additionally correspond to peptide sequences present in non enveloped and non-viral organisms. Such peptides may exhibit antifusogenic activity, antiviral activity, most particularly antiviral activity which is specific to the virus in which their native sequences are found, or may exhibit an ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are peptides whose amino acid sequences are comprised of the amino acid sequences of peptide regions of, for example, other (*i.e.*, other than HIV-1<sub>LAI</sub>) viruses that correspond to the gp41 peptide region from which DP178 (SEQ ID:1) was derived. Such viruses may include, but are not limited to, other HIV-1 isolates and HIV-2 isolates. DP178 analogs derived from the corresponding gp41 peptide region of other (*i.e.*, non HIV-1<sub>LAI</sub>) HIV-1 isolates may include, for example, peptide sequences as shown below.

NH<sub>2</sub>-YTNTIYTLLEESQNQQEKNEQEELLELDKWASLWNWF-COOH (DP-185; SEQ ID:3);

NH<sub>2</sub>-YTGIIYNLLEESQNQQEKNEQEELLELDKWANLWNWF-COOH (SEQ ID:4);

NH<sub>2</sub>-YTSLIYSLLEKSQIQQEKNEQEELLELDKWASLWNWF-COOH (SEQ ID:5).

SEQ ID:3 (DP-185), SEQ ID:4, and SEQ ID:5 are derived from HIV-1<sub>SF2</sub>, HIV-1<sub>RF</sub>, and HIV-1<sub>MN</sub> isolates, respectively. Underlined amino acid residues refer to those residues that differ from the corresponding position in the DP178 (SEQ ID:1) peptide. One such



DP178 analog, DP-185 (SEQ ID:3), is described in the Example presented in Section 6, below, where it is demonstrated that DP-185 (SEQ ID:3) exhibits antiviral activity. The DP178 analogs of the invention may also include truncations, as described above. Further, the  
 5 analogs of the invention modifications such those described for DP178 analogs in Section 5.1., above. It is preferred that the DP178 analogs of the invention represent peptides whose amino acid sequences correspond to the DP178 region of the gp41  
 10 protein, it is also contemplated that the peptides of the invention may, additionally, include amino sequences, ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178  
 15 amino acid sequence.

Striking similarities, as shown in FIG. 1, exist within the regions of HIV-1 and HIV-2 isolates which correspond to the DP178 sequence. A DP178 analog derived from the HIV-2<sub>NIH2</sub> isolate has the 36 amino acid  
 20 sequence (reading from amino to carboxy terminus):

NH<sub>2</sub>-LEANISQSLEQAQIQQEKMYELQKLNSWDVFTNWL-COOH (SEQ ID:7)

Table III and Table IV show some possible truncations  
 25 of the HIV-2<sub>NIH2</sub> DP178 analog, which may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide). Peptide sequences in these tables are listed from amino (left) to carboxy (right)  
 30 terminus. "X" may represent an amino group (-NH<sub>2</sub>) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-  
 35 fluorenylmethoxy-carbonyl (Fmoc) group; or a



covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached  
5 macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

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TABLE IIIHIV-2<sub>NDZ</sub> DP178 analog carboxy truncations.

X-LEA-Z  
 X-LEAN-Z  
 X-LEANI-Z  
 X-LEANIS-Z  
 5 X-LEANISQ-Z  
 X-LEANISQS-Z  
 X-LEANISQSL-Z  
 X-LEANISQSLE-Z  
 X-LEANISQSLEQ-Z  
 X-LEANISQSLEQA-Z  
 X-LEANISQSLEQAQ-Z  
 10 X-LEANISQSLEQAQI-Z  
 X-LEANISQSLEQAQIQ-Z  
 X-LEANISQSLEQAQIQQ-Z  
 X-LEANISQSLEQAQIQQE-Z  
 X-LEANISQSLEQAQIQQEK-Z  
 X-LEANISQSLEQAQIQQEKN-Z  
 X-LEANISQSLEQAQIQQEKNM-Z  
 X-LEANISQSLEQAQIQQEKNMY-Z  
 15 X-LEANISQSLEQAQIQQEKNMYE-Z  
 X-LEANISQSLEQAQIQQEKNMYEL-Z  
 X-LEANISQSLEQAQIQQEKNMYELQ-Z  
 X-LEANISQSLEQAQIQQEKNMYELQK-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKL-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLN-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNS-Z  
 20 X-LEANISQSLEQAQIQQEKNMYELQKLNSW-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWD-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDV-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVF-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFT-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTN-Z  
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNW-Z  
 25 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxyl, dansyl, or  
 30 T-butyloxycarbonyl; an acetyl group; a 9-  
 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
 T-butyloxycarbonyl group; a macromolecular carrier  
 35 group including but not limited to lipid-fatty acid  
 conjugates, polyethylene glycol, or carbohydrates.



TABLE IVHIV-2<sub>ND12</sub> DP178 analog amino truncations.

	X-NWL-Z
	X-TNWL-Z
	X-FTNWL-Z
5	X-VFTNWL-Z
	X-DVFTNWL-Z
	X-WDVFTNWL-Z
	X-SWDVFTNWL-Z
	X-NSWDVFTNWL-Z
	X-LNSWDVFTNWL-Z
	X-KLNSWDVFTNWL-Z
	X-QKLNSWDVFTNWL-Z
10	X-LQKLNSWDVFTNWL-Z
	X-ELQKLNSWDVFTNWL-Z
	X-YELQKLNSWDVFTNWL-Z
	X-MYELQKLNSWDVFTNWL-Z
	X-NMYELQKLNSWDVFTNWL-Z
	X-KNMYELQKLNSWDVFTNWL-Z
	X-EKNMYELQKLNSWDVFTNWL-Z
	X-QEKNMYELQKLNSWDVFTNWL-Z
15	X-QQEKNMYELQKLNSWDVFTNWL-Z
	X-IQQEKNMYELQKLNSWDVFTNWL-Z
	X-QIQQEKNMYELQKLNSWDVFTNWL-Z
	X-AQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-QAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-EQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-LEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
20	X-SLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-QSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-SQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-ISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-NISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-ANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-EANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
25	X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.



DP178 and DP107 analogs are recognized or identified, for example, by utilizing one or more of the 107x178x4, ALLMOTI5 or PLZIP computer-assisted search strategies described and demonstrated, below, in the Examples presented in Sections 9 through 16 and 19 through 25. The search strategy identifies additional peptide regions which are predicted to have structural and/or amino acid sequence features similar to those of DP107 and/or DP178.

The search strategies are described fully, below, in the Example presented in Section 9. While this search strategy is based, in part, on a primary amino acid motif deduced from DP107 and DP178, it is not based solely on searching for primary amino acid sequence homologies, as such protein sequence homologies exist within, but not between major groups of viruses. For example, primary amino acid sequence homology is high within the TM protein of different strains of HIV-1 or within the TM protein of different isolates of simian immunodeficiency virus (SIV). Primary amino acid sequence homology between HIV-1 and SIV, however, is low enough so as not to be useful. It is not possible, therefore, to find peptide regions similar to DP107 or DP178 within other viruses, or within non-viral organisms, whether structurally, or otherwise, based on primary sequence homology, alone.

Further, while it would be potentially useful to identify primary sequence arrangements of amino acids based on, for example, the physical chemical characteristics of different classes of amino acids rather than based on the specific amino acids themselves, such search strategies have, until now, proven inadequate. For example, a computer algorithm designed by Lupas et al. to identify coiled-coil propensities of regions within proteins (Lupas, A., et al., 1991 Science 252:1162-1164) is inadequate for



identifying protein regions analogous to DP107 or DP178.

Specifically, analysis of HIV-1 gp160 (containing both gp120 and gp41) using the Lupas algorithm does not identify the coiled-coil region within DP107. It  
5 does, however, identify a region within DP178 beginning eight amino acids N-terminal to the start of DP178 and ending eight amino acids from the C-terminus. The DP107 peptide has been shown  
10 experimentally to form a stable coiled coil. A search based on the Lupas search algorithm, therefore, would not have identified the DP107 coiled-coil region. Conversely, the Lupas algorithm identified the DP178 region as a potential coiled-coil motif. However, the peptide derived from the DP178 region failed to form a  
15 coiled coil in solution.

A possible explanation for the inability of the Lupas search algorithm to accurately identify coiled-coil sequences within the HIV-1 TM, is that the Lupas algorithm is based on the structure of coiled coils  
20 from proteins that are not structurally or functionally similar to the TM proteins of viruses, antiviral peptides (e.g. DP107 and DP178) of which are an object of this invention.

The computer search strategy of the invention, as  
25 demonstrated in the Examples presented below, in Sections 9 through 16 and 19 through 25, successfully identifies regions of proteins similar to DP107 or DP178. This search strategy was designed to be used with a commercially-available sequence database  
30 package, preferably PC/Gene.

A series of search motifs, the 107x178x4, ALLMOTI5 and PLZIP motifs, were designed and engineered to range in stringency from strict to  
35 broad, as discussed in this Section and in Section 9, with 107x178x4 being preferred. The sequences



identified via such search motifs, such as those listed in Tables V-XIV, below, potentially exhibit antifusogenic, such as antiviral, activity, may additionally be useful in the identification of antifusogenic, such as antiviral, compounds, and are intended to be within the scope of the invention.

Coiled-coiled sequences are thought to consist of heptad amino acid repeats. For ease of description, the amino acid positions within the heptad repeats are sometimes referred to as A through G, with the first position being A, the second B, etc. The motifs used to identify DP107-like and DP178-like sequences herein are designed to specifically search for and identify such heptad repeats. In the descriptions of each of the motifs described, below, amino acids enclosed by brackets, i.e., [], designate the only amino acid residues that are acceptable at the given position, while amino acids enclosed by braces, i.e., {}, designate the only amino acids which are unacceptable at the given heptad position. When a set of bracketed or braced amino acids is followed by a number in parentheses i.e., (), it refers to the number of subsequent amino acid positions for which the designated set of amino acids hold, e.g., a (2) means "for the next two heptad amino acid positions".

The ALLMOTIS is written as follows:

```
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
```

Translating this motif, it would read: "at the first (A) position of the heptad, any amino acid residue except C, D, G, H, or P is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, or P is acceptable, at the fourth heptad position (D), any amino acid residue except C,



D, G, H, or P is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, or P is acceptable. This motif is designed to search for five consecutive heptad repeats (thus the repeat of the first line five times), meaning that it searches for 35-mer sized peptides. It may also be designed to search for 28-mers, by only repeating the initial motif four times. With respect to the ALLMOTI5 motif, a 35-mer search is preferred. Those viral (non-bacteriophage) sequences identified via such an ALLMOTI5 motif are listed in Table V, below, at the end of this Section. The viral sequences listed in Table V potentially exhibit antiviral activity, may be useful in the identification of antiviral compounds, and are intended to be within the scope of the invention. In those instances wherein a single gene exhibits greater than one sequence recognized by the ALLMOTI5 search motif, the amino acid residue numbers of these sequences are listed under "Area 2", Area 3", etc. This convention is used for each of the Tables listed, below, at the end of this Section.

The 107x178x4 motif is written as follows:

[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-  
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-  
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-  
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-

Translating this motif, it would read: "at the first (A) position of the heptad, only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, M or P is acceptable, at the fourth position (D), only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, M or P is acceptable. This motif is designed to search for



four consecutive heptad repeats (thus the repeat of the first line four times), meaning that it searches for 28-mer sized peptides. It may also be designed to search for 35-mers, by repeating the initial motif five times. With respect to the 107x178x4 motif, a 28-mer search is preferred.

Those viral (non-bacteriophage) sequences identified via such a 107x178x4 motif are listed in Table VI, below, at the end of this Section, with those viral (non-bacteriophage) sequences listed in Table VII, below at the end of this Section, being preferred.

The 107x178x4 search motif was also utilized to identify non-viral procaryotic protein sequences, as listed in Table VIII, below, at the end of this Section. Further, this search motif was used to reveal a number of human proteins. The results of this human protein 107x178x4 search is listed in Table IX, below, at the end of this Section. The sequences listed in Tables VIII and IX, therefore, reveal peptides which may be useful as antifusogenic compounds or in the identification of antifusogenic compounds, and are intended to be within the scope of the invention.

The PLZIP series of motifs are as listed in FIG. 19. These motifs are designed to identify leucine zipper coiled-coil like heptads wherein at least one proline residue is present at some predefined distance N-terminal to the repeat. These PLZIP motifs find regions of proteins with similarities to HIV-1 DP178 generally located just N-terminal to the transmembrane anchor. These motifs may be translated according to the same convention described above. Each line depicted in FIG. 19 represents a single, complete search motif. "X" in these motifs refers to any amino acid residue. In instances wherein a motif contains



two numbers within parentheses, this refers to a variable number of amino acid residues. For example, X (1,12) is translated to "the next one to twelve amino acid residues, inclusive, may be any amino acid".

5       Tables X through XIV, below, at the end of this Section, list sequences identified via searches conducted with such PLZIP motifs. Specifically, Table X lists viral sequences identified via PCTLZIP, P1CTLZIP and P2CTLZIP search motifs, Table XI lists  
10       viral sequences identified via P3CTLZIP, P4CTLZIP, P5CTLZIP and P6CTLZIP search motifs, Table XII lists viral sequences identified via P7CTLZIP, P8CTLZIP and P9CTLZIP search motifs, Table XIII lists viral sequences identified via P12LZIPC searches and Table  
15       XIV lists viral sequences identified via P23TLZIPC search motifs. The viral sequences listed in these tables represent peptides which potentially exhibit antiviral activity, may be useful in the identification of antiviral compounds, and are  
20       intended to be within the scope of the invention.

      The Examples presented in Sections 17, 18, 26 and 27 below, demonstrate that viral sequences identified via the motif searches described herein identify  
25       substantial antiviral characteristics. Specifically, the Example presented in Section 17 describes peptides with anti-respiratory syncytial virus activity, the Example presented in Section 18 describes peptides with anti-parainfluenza virus activity, the Example presented in Section 26 describes peptides with anti-  
30       measles virus activity and the Example presented in Section 27 describes peptides with anti-simian immunodeficiency virus activity.

      The DP107 and DP178 analogs may, further, contain any of the additional groups described for DP178,  
35       above, in Section 5.1. For example, these peptides



may include any of the additional amino-terminal groups as described above for "X" groups, and may also include any of the carboxy-terminal groups as described, above, for "Z" groups.

5        Additionally, truncations of the identified DP107 and DP178 peptides are among the peptides of the invention. Further, such DP107 and DP178 analogs and DP107/DP178 analog truncations may exhibit one or more amino acid substitutions, insertion, and/or deletions. The DP178 analog amino acid substitutions, insertions  
10       and deletions, are as described, above, for DP178-like peptides in Section 5.1. The DP-107 analog amino acid substitutions, insertions and deletions are also as described, above, for DP107-like peptides in Section  
15       5.2.

15       Tables XV through XXII, below, present representative examples of such DP107/DP178 truncations. Specifically, Table XV presents Respiratory Syncytial Virus F1 region DP107 analog carboxy truncations, Table XVI presents Respiratory  
20       Syncytial Virus F1 region DP107 analog amino truncations, Table XVII presents Respiratory Syncytial Virus F1 region DP178 analog carboxy truncations, Table XVIII presents Respiratory Syncytial Virus F1 region DP178 analog amino truncations, Table XIX  
25       presents Human Parainfluenza Virus 3 F1 region DP178 analog carboxy truncations, Table XX presents Human Parainfluenza Virus 3 F1 region DP178 analog amino truncations, Table XXI presents Human Parainfluenza Virus 3 F1 region DP107 analog carboxy truncations and  
30       Table XXII presents Human Parainfluenza Virus 3 F1 region DP107 analog amino truncations. Further, Table XXIII, below, presents DP107/DP178 analogs and analog truncations which exhibit substantial antiviral activity. These antiviral peptides are grouped  
35       according to the specific virus which they inhibit,



including respiratory syncytial virus, human  
parainfluenza virus 3, simian immunodeficiency virus  
and measles virus.

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TABLE V

ALLMOTIS SEARCH RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS



[illegible]



PGENE		ALLNOTES	ABCA1	ABCA2	ABCA3	ABCA4	ABCA5	ABCA6	ABCA7	ABCA8	ABCA9	ABCA10	ABCA11	ABCA12	ABCA13	ABCA14	ABCA15	ABCA16	ABCA17	ABCA18	ABCA19	ABCA20	ABCA21	ABCA22	ABCA23	ABCA24	ABCA25	ABCA26	ABCA27	ABCA28	ABCA29	ABCA30	ABCA31	ABCA32	ABCA33	ABCA34	ABCA35	ABCA36	ABCA37	ABCA38	ABCA39	ABCA40	ABCA41	ABCA42	ABCA43	ABCA44	ABCA45	ABCA46	ABCA47	ABCA48	ABCA49	ABCA50	ABCA51	ABCA52	ABCA53	ABCA54	ABCA55	ABCA56	ABCA57	ABCA58	ABCA59	ABCA60	ABCA61	ABCA62	ABCA63	ABCA64	ABCA65	ABCA66	ABCA67	ABCA68	ABCA69	ABCA70	ABCA71	ABCA72	ABCA73	ABCA74	ABCA75	ABCA76	ABCA77	ABCA78	ABCA79	ABCA80	ABCA81	ABCA82	ABCA83	ABCA84	ABCA85	ABCA86	ABCA87	ABCA88	ABCA89	ABCA90	ABCA91	ABCA92	ABCA93	ABCA94	ABCA95	ABCA96	ABCA97	ABCA98	ABCA99	ABCA100	ABCA101	ABCA102	ABCA103	ABCA104	ABCA105	ABCA106	ABCA107	ABCA108	ABCA109	ABCA110	ABCA111	ABCA112	ABCA113	ABCA114	ABCA115	ABCA116	ABCA117	ABCA118	ABCA119	ABCA120	ABCA121	ABCA122	ABCA123	ABCA124	ABCA125	ABCA126	ABCA127	ABCA128	ABCA129	ABCA130	ABCA131	ABCA132	ABCA133	ABCA134	ABCA135	ABCA136	ABCA137	ABCA138	ABCA139	ABCA140	ABCA141	ABCA142	ABCA143	ABCA144	ABCA145	ABCA146	ABCA147	ABCA148	ABCA149	ABCA150	ABCA151	ABCA152	ABCA153	ABCA154	ABCA155	ABCA156	ABCA157	ABCA158	ABCA159	ABCA160	ABCA161	ABCA162	ABCA163	ABCA164	ABCA165	ABCA166	ABCA167	ABCA168	ABCA169	ABCA170	ABCA171	ABCA172	ABCA173	ABCA174	ABCA175	ABCA176	ABCA177	ABCA178	ABCA179	ABCA180	ABCA181	ABCA182	ABCA183	ABCA184	ABCA185	ABCA186	ABCA187	ABCA188	ABCA189	ABCA190	ABCA191	ABCA192	ABCA193	ABCA194	ABCA195	ABCA196	ABCA197	ABCA198	ABCA199	ABCA200	ABCA201	ABCA202	ABCA203	ABCA204	ABCA205	ABCA206	ABCA207	ABCA208	ABCA209	ABCA210	ABCA211	ABCA212	ABCA213	ABCA214	ABCA215	ABCA216	ABCA217	ABCA218	ABCA219	ABCA220	ABCA221	ABCA222	ABCA223	ABCA224	ABCA225	ABCA226	ABCA227	ABCA228	ABCA229	ABCA230	ABCA231	ABCA232	ABCA233	ABCA234	ABCA235	ABCA236	ABCA237	ABCA238	ABCA239	ABCA240	ABCA241	ABCA242	ABCA243	ABCA244	ABCA245	ABCA246	ABCA247	ABCA248	ABCA249	ABCA250	ABCA251	ABCA252	ABCA253	ABCA254	ABCA255	ABCA256	ABCA257	ABCA258	ABCA259	ABCA260	ABCA261	ABCA262	ABCA263	ABCA264	ABCA265	ABCA266	ABCA267	ABCA268	ABCA269	ABCA270	ABCA271	ABCA272	ABCA273	ABCA274	ABCA275	ABCA276	ABCA277	ABCA278	ABCA279	ABCA280	ABCA281	ABCA282	ABCA283	ABCA284	ABCA285	ABCA286	ABCA287	ABCA288	ABCA289	ABCA290	ABCA291	ABCA292	ABCA293	ABCA294	ABCA295	ABCA296	ABCA297	ABCA298	ABCA299	ABCA300	ABCA301	ABCA302	ABCA303	ABCA304	ABCA305	ABCA306	ABCA307	ABCA308	ABCA309	ABCA310	ABCA311	ABCA312	ABCA313	ABCA314	ABCA315	ABCA316	ABCA317	ABCA318	ABCA319	ABCA320	ABCA321	ABCA322	ABCA323	ABCA324	ABCA325	ABCA326	ABCA327	ABCA328	ABCA329	ABCA330	ABCA331	ABCA332	ABCA333	ABCA334	ABCA335	ABCA336	ABCA337	ABCA338	ABCA339	ABCA340	ABCA341	ABCA342	ABCA343	ABCA344	ABCA345	ABCA346	ABCA347	ABCA348	ABCA349	ABCA350	ABCA351	ABCA352	ABCA353	ABCA354	ABCA355	ABCA356	ABCA357	ABCA358	ABCA359	ABCA360	ABCA361	ABCA362	ABCA363	ABCA364	ABCA365	ABCA366	ABCA367	ABCA368	ABCA369	ABCA370	ABCA371	ABCA372	ABCA373	ABCA374	ABCA375	ABCA376	ABCA377	ABCA378	ABCA379	ABCA380	ABCA381	ABCA382	ABCA383	ABCA384	ABCA385	ABCA386	ABCA387	ABCA388	ABCA389	ABCA390	ABCA391	ABCA392	ABCA393	ABCA394	ABCA395	ABCA396	ABCA397	ABCA398	ABCA399	ABCA400	ABCA401	ABCA402	ABCA403	ABCA404	ABCA405	ABCA406	ABCA407	ABCA408	ABCA409	ABCA410	ABCA411	ABCA412	ABCA413	ABCA414	ABCA415	ABCA416	ABCA417	ABCA418	ABCA419	ABCA420	ABCA421	ABCA422	ABCA423	ABCA424	ABCA425	ABCA426	ABCA427	ABCA428	ABCA429	ABCA430	ABCA431	ABCA432	ABCA433	ABCA434	ABCA435	ABCA436	ABCA437	ABCA438	ABCA439	ABCA440	ABCA441	ABCA442	ABCA443	ABCA444	ABCA445	ABCA446	ABCA447	ABCA448	ABCA449	ABCA450	ABCA451	ABCA452	ABCA453	ABCA454	ABCA455	ABCA456	ABCA457	ABCA458	ABCA459	ABCA460	ABCA461	ABCA462	ABCA463	ABCA464	ABCA465	ABCA466	ABCA467	ABCA468	ABCA469	ABCA470	ABCA471	ABCA472	ABCA473	ABCA474	ABCA475	ABCA476	ABCA477	ABCA478	ABCA479	ABCA480	ABCA481	ABCA482	ABCA483	ABCA484	ABCA485	ABCA486	ABCA487	ABCA488	ABCA489	ABCA490	ABCA491	ABCA492	ABCA493	ABCA494	ABCA495	ABCA496	ABCA497	ABCA498	ABCA499	ABCA500	ABCA501	ABCA502	ABCA503	ABCA504	ABCA505	ABCA506	ABCA507	ABCA508	ABCA509	ABCA510	ABCA511	ABCA512	ABCA513	ABCA514	ABCA515	ABCA516	ABCA517	ABCA518	ABCA519	ABCA520	ABCA521	ABCA522	ABCA523	ABCA524	ABCA525	ABCA526	ABCA527	ABCA528	ABCA529	ABCA530	ABCA531	ABCA532	ABCA533	ABCA534	ABCA535	ABCA536	ABCA537	ABCA538	ABCA539	ABCA540	ABCA541	ABCA542	ABCA543	ABCA544	ABCA545	ABCA546	ABCA547	ABCA548	ABCA549	ABCA550	ABCA551	ABCA552	ABCA553	ABCA554	ABCA555	ABCA556	ABCA557	ABCA558	ABCA559	ABCA560	ABCA561	ABCA562	ABCA563	ABCA564	ABCA565	ABCA566	ABCA567	ABCA568	ABCA569	ABCA570	ABCA571	ABCA572	ABCA573	ABCA574	ABCA575	ABCA576	ABCA577	ABCA578	ABCA579	ABCA580	ABCA581	ABCA582	ABCA583	ABCA584	ABCA585	ABCA586	ABCA587	ABCA588	ABCA589	ABCA590	ABCA591	ABCA592	ABCA593	ABCA594	ABCA595	ABCA596	ABCA597	ABCA598	ABCA599	ABCA600	ABCA601	ABCA602	ABCA603	ABCA604	ABCA605	ABCA606	ABCA607	ABCA608	ABCA609	ABCA610	ABCA611	ABCA612	ABCA613	ABCA614	ABCA615	ABCA616	ABCA617	ABCA618	ABCA619	ABCA620	ABCA621	ABCA622	ABCA623	ABCA624	ABCA625	ABCA626	ABCA627	ABCA628	ABCA629	ABCA630	ABCA631	ABCA632	ABCA633	ABCA634	ABCA635	ABCA636	ABCA637	ABCA638	ABCA639	ABCA640	ABCA641	ABCA642	ABCA643	ABCA644	ABCA645	ABCA646	ABCA647	ABCA648	ABCA649	ABCA650	ABCA651	ABCA652	ABCA653	ABCA654	ABCA655	ABCA656	ABCA657	ABCA658	ABCA659	ABCA660	ABCA661	ABCA662	ABCA663	ABCA664	ABCA665	ABCA666	ABCA667	ABCA668	ABCA669	ABCA670	ABCA671	ABCA672	ABCA673	ABCA674	ABCA675	ABCA676	ABCA677	ABCA678	ABCA679	ABCA680	ABCA681	ABCA682	ABCA683	ABCA684	ABCA685	ABCA686	ABCA687	ABCA688	ABCA689	ABCA690	ABCA691	ABCA692	ABCA693	ABCA694	ABCA695	ABCA696	ABCA697	ABCA698	ABCA699	ABCA700	ABCA701	ABCA702	ABCA703	ABCA704	ABCA705	ABCA706	ABCA707	ABCA708	ABCA709	ABCA710	ABCA711	ABCA712	ABCA713	ABCA714	ABCA715	ABCA716	ABCA717	ABCA718	ABCA719	ABCA720	ABCA721	ABCA722	ABCA723	ABCA724	ABCA725	ABCA726	ABCA727	ABCA728	ABCA729	ABCA730	ABCA731	ABCA732	ABCA733	ABCA734	ABCA735	ABCA736	ABCA737	ABCA738	ABCA739	ABCA740	ABCA741	ABCA742	ABCA743	ABCA744	ABCA745	ABCA746	ABCA747	ABCA748	ABCA749	ABCA750	ABCA751	ABCA752	ABCA753	ABCA754	ABCA755	ABCA756	ABCA757	ABCA758	ABCA759	ABCA760	ABCA761	ABCA762	ABCA763	ABCA764	ABCA765	ABCA766	ABCA767	ABCA768	ABCA769	ABCA770	ABCA771	ABCA772	ABCA773	ABCA774	ABCA775	ABCA776	ABCA777	ABCA778	ABCA779	ABCA780	ABCA781	ABCA782	ABCA783	ABCA784	ABCA785	ABCA786	ABCA787	ABCA788	ABCA789	ABCA790	ABCA791	ABCA792	ABCA793	ABCA794	ABCA795	ABCA796	ABCA797	ABCA798	ABCA799	ABCA800	ABCA801	ABCA802	ABCA803	ABCA804	ABCA805	ABCA806	ABCA807	ABCA808	ABCA809	ABCA810	ABCA811	ABCA812	ABCA813	ABCA814	ABCA815	ABCA816	ABCA817	ABCA818	ABCA819	ABCA820	ABCA821	ABCA822	ABCA823	ABCA824	ABCA825	ABCA826	ABCA827	ABCA828	ABCA829	ABCA830	ABCA831	ABCA832	ABCA833	ABCA834	ABCA835	ABCA836	ABCA837	ABCA838	ABCA839	ABCA840	ABCA841	ABCA842	ABCA843	ABCA844	ABCA845	ABCA846	ABCA847	ABCA848	ABCA849	ABCA850	ABCA851	ABCA852	ABCA853	ABCA854	ABCA855	ABCA856	ABCA857	ABCA858	ABCA859	ABCA860	ABCA861	ABCA862	ABCA863	ABCA864	ABCA865	ABCA866	ABCA867	ABCA868	ABCA869	ABCA870	ABCA871	ABCA872	ABCA873	ABCA874	ABCA875	ABCA876	ABCA877	ABCA878	ABCA879	ABCA880	ABCA881	ABCA882	ABCA883	ABCA884	ABCA885	ABCA886	ABCA887	ABCA888	ABCA889	ABCA890	ABCA891	ABCA892	ABCA893	ABCA894	ABCA895	ABCA896	ABCA897	ABCA898	ABCA899	ABCA900	ABCA901	ABCA902	ABCA903	ABCA904	ABCA905	ABCA906	ABCA907	ABCA908	ABCA909	ABCA910	ABCA911	ABCA912	ABCA913	ABCA914	ABCA915	ABCA916	ABCA917	ABCA918	ABCA919	ABCA920	ABCA921	ABCA922	ABCA923	ABCA924	ABCA925	ABCA926	ABCA927	ABCA928	ABCA929	ABCA930	ABCA931	ABCA932	ABCA933	ABCA934	ABCA935	ABCA936	ABCA937	ABCA938	ABCA939	ABCA940	ABCA941	ABCA942	ABCA943	ABCA944	ABCA945	ABCA946	ABCA947	ABCA948	ABCA949	ABCA950	ABCA951	ABCA952	ABCA953	ABCA954	ABCA955	ABCA956	ABCA957	ABCA958	ABCA959	ABCA960	ABCA961	ABCA962	ABCA963	ABCA964	ABCA965	ABCA966	ABCA967	ABCA968	ABCA969	ABCA970	ABCA971	ABCA972	ABCA973	ABCA974	ABCA975	ABCA976	ABCA977	ABCA978	ABCA979	ABCA980	ABCA981	ABCA982	ABCA983	ABCA984	ABCA985	ABCA986	ABCA987	ABCA988	ABCA989	ABCA990	ABCA991	ABCA992	ABCA993	ABCA994	ABCA995	ABCA996	ABCA997	ABCA998	ABCA999	ABCA1000
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[illegible]



FIGURE	ALLIQUOT	AB Virus (no bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
FIGURE 1	PROTEIN	VIRUS	685-141							
FIGURE 2	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 13	207-240							
FIGURE 3	DNA POLYMERASE	CHORISTOMELA BIENNIS ENTOMONOXVIRUS	342-384							
FIGURE 4	DNA POLYMERASE	CHLORELLA VIRUS NY-2A	247-284							
FIGURE 5	DNA POLYMERASE	PARARECUM BURSARIA CHLORELLA VIRUS 1	17-31	371-412						
FIGURE 6	DNA POLYMERASE	FOVLPX VIRUS	313-352	1031-1074						
FIGURE 7	DNA POLYMERASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	5-39							
FIGURE 8	DNA POLYMERASE	DUCK HEPATITIS B VIRUS	5-39							
FIGURE 9	DNA POLYMERASE	DUCK HEPATITIS B VIRUS (STRAIN CHINA)	5-39							
FIGURE 10	DNA POLYMERASE	DUCK HEPATITIS B VIRUS (WHITE SHANGHAI DUCK ISOLATE 5)	201-235							
FIGURE 11	DNA POLYMERASE	GROUND SQUID HEPATITIS VIRUS	5-39	334-383						
FIGURE 12	DNA POLYMERASE	HEKON HEPATITIS B VIRUS	201-235							
FIGURE 13	DNA POLYMERASE	HEPATITIS B VIRUS (SUBTYPE AYW)	201-235							
FIGURE 14	DNA POLYMERASE	HEPATITIS B VIRUS (SUBTYPE ADYM)	511-559							
FIGURE 15	DNA POLYMERASE	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	511-559							
FIGURE 16	DNA POLYMERASE	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN ANGELOTT)	511-559							
FIGURE 17	DNA POLYMERASE	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN KOS)	511-559							
FIGURE 18	DNA POLYMERASE	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN SC16)	511-559							
FIGURE 19	DNA POLYMERASE	HERPES SIMPLEX VIRUS (TYPE 2/STRAIN 186)	512-560							
FIGURE 20	DNA POLYMERASE	HERPES SIMPLEX VIRUS (TYPE 2/STRAIN AD47)	494-528							
FIGURE 21	DNA POLYMERASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD47)	33-47	321-364	206-749					
FIGURE 22	DNA POLYMERASE	ACTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS)	595-646							
FIGURE 23	DNA POLYMERASE	AUTOGRAPIA CALIFORNICA NUCLEAR POLYDIOSIS VIRUS	627-683	770-118						
FIGURE 24	DNA POLYMERASE	VACCINIA VIRUS (STRAIN COPIERAGEN)	627-683	770-118	828-862					
FIGURE 25	DNA POLYMERASE	VACCINIA VIRUS (STRAIN WR)	628-682	769-817	827-861					
FIGURE 26	DNA POLYMERASE	VARIOLA VIRUS	473-532							
FIGURE 27	DNA POLYMERASE	VARIOLA-ZOSTER VIRUS (STRAIN DUMAS)	385-376							
FIGURE 28	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 1	290-331							
FIGURE 29	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 59	290-331							
FIGURE 30	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 7	290-331							
FIGURE 31	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 8	290-331							
FIGURE 32	DNA POLYMERASE	WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE)	290-331							
FIGURE 33	DNA POLYMERASE	HEPATITIS B VIRUS (SUBTYPE AYW)	201-235							
FIGURE 34	DNA POLYMERASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB-47)	135-169							
FIGURE 35	DNA POLYMERASE	HEPESVIRUS SAIMIRI (STRAIN 11)	179-223							
FIGURE 36	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 41	107-141							
FIGURE 37	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 40	102-166							
FIGURE 38	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 2	102-137							
FIGURE 39	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 3	102-137							
FIGURE 40	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 11	96-131							
FIGURE 41	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 12	100-134							
FIGURE 42	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 40	100-134							
FIGURE 43	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 41	119-173							
FIGURE 44	DNA POLYMERASE	MOUSE ADENOVIRUS TYPE 1	2-39							
FIGURE 45	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 2	2-39							
FIGURE 46	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 3	2-39							
FIGURE 47	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 7	7-48							
FIGURE 48	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 13	70-107							
FIGURE 49	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 33	123-169							
FIGURE 50	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 35	10-44							
FIGURE 51	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 3	10-44							
FIGURE 52	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 3	123-157							
FIGURE 53	DNA POLYMERASE	EPSTEIN-BARR VIRUS (STRAIN 951-8)	487-531							
FIGURE 54	DNA POLYMERASE	EPSTEIN-BARR VIRUS (STRAIN 895-9)	23-71	103-341						
FIGURE 55	DNA POLYMERASE	VARIOLA VIRUS								
FIGURE 56	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 57	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 58	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 59	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 60	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 61	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 62	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 63	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 64	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 65	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 66	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 67	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 68	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 69	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 70	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 71	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 72	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 73	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 74	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 75	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 76	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 77	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 78	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 79	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 80	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 81	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 82	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 83	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 84	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 85	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 86	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 87	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 88	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 89	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 90	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 91	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 92	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 93	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 94	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 95	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 96	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 97	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 98	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 99	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								
FIGURE 100	DNA POLYMERASE	EARLY TRANSCRIPTION FACTOR 79 KD SUBUNIT								



[illegible]



[illegible]



PCGENE	ALLOTTIS	ALL Viruses (see bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PROTEIN	PROTEIN	VIRUS								
ENVELOPE POLYPROTEIN GP160 PRECURSOR	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (AGN1 ISOLATE)	594-428	608-433						
ENVELOPE POLYPROTEIN GP160 PRECURSOR	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE AGN1 CLONE OR)	557-391	535-407	792-840					
ENVELOPE POLYPROTEIN GP160 PRECURSOR	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (TVG-1 ISOLATE)	644-398	644-492	796-833					
ENVELOPE POLYPROTEIN GP160 PRECURSOR	ENVELOPE POLYPROTEIN GP160 PRECURSOR	CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIVCPZ2)	553-391	535-384	803-837					
ENVELOPE POLYPROTEIN GP160 PRECURSOR	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE GRI)	566-654	677-723						
ENVELOPE POLYPROTEIN GP160 PRECURSOR	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (DMS12-83 ISOLATE)	114-151	465-596	635-613	809-844				
ENVELOPE POLYPROTEIN GP160 PRECURSOR	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (DMS1 ISOLATE)	114-151	465-596	635-613	809-844				
ENVELOPE POLYPROTEIN GP160 PRECURSOR	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (KAW ISOLATE)	464-505	549-612	635-724					
ENVELOPE POLYPROTEIN GP160 PRECURSOR	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (K78 ISOLATE)	464-505	549-612	635-724					
ENVELOPE POLYPROTEIN GP160 PRECURSOR	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (F3465/816 ISOLATE)	464-509	517-616	616-728	812-853				
ENVELOPE POLYPROTEIN GP160 PRECURSOR	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SIMIAN IMMUNODEFICIENCY VIRUS (P18/0C11 ISOLATE)	470-513	521-620	642-722	811-848				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	SQUID LENTIVIRUS (SQUID-11)	409-466							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	SIMIAN RETROVIRUS SV4-1	409-475							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	VIRAL LENTIVIRUS (STRAIN 1314)	21-62	184-222	637-740	773-802				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	VIRAL LENTIVIRUS (STRAIN 1314/7 CLONE LV1-1K531)	21-62	184-222	643-740	780-814				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	VIRAL LENTIVIRUS (STRAIN 1314/7 CLONE LV1-1K532)	21-62	184-222	643-748	782-818				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	AVIAN ERYTHROBLASTOSIS VIRUS (STRAIN ES4)	106-140							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FOWLPOX VIRUS (STRAIN TP-1)	190-224	533-587						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	SHOEPOX VIRUS (STRAIN KASZAI)	37-71	267-340	350-387					
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	21-71	307-341						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN WR)	21-71	307-341						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	32-97	174-208						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	32-97	174-208						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	80-114							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	80-114							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	PSEUDOTABES VIRUS (STRAIN NIA-3)	82-120							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	VACCINIA-ZOSTER VIRUS (STRAIN DUNIAS)	109-157	182-237	342-383					
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 40	182-237							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 41	182-237							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 3	158-194							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 7	176-210							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 40	101-332							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN ADENOVIRUS TYPE 41	220-266							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	BOVINE ADENOVIRUS TYPE 3	181-215	585-626						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FIBRILIN OSTEOGENESIS VIRUS	131-169							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	AVIAN RETROVIRUS M2N	109-152							
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FBI MYRINE OSTEOGENESIS VIRUS	153-193							



[illegible]



[illegible]



[illegible]



PCGENE	ALLHOTIS	ALL VITRES (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
PHENIA_INCH1	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CANISSIPPO)	470-538					
PHENIA_INCH2	HEMAGGLUTININ	INFLUENZA C VIRUS (STRAIN CANABAB2)	470-538					
PHENIA_INCH3	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CPGIOEING1081)	471-539					
PHENIA_INCH4	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CPGIOEING11541)	471-539					
PHENIA_INCH5	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CPGIOEING11942)	471-539					
PHENIA_INCH6	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CPGIOEING12107)	471-539					
PHENIA_INCH7	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CPGIOEING12107)	471-539					
PHENIA_INCH8	HEMAGGLUTININ PRECURSOR	MEASLES VIRUS (STRAIN EDONSTOM)	46-90					
PHENIA_INCH9	HEMAGGLUTININ-NEURAMINIDASE	MEASLES VIRUS (STRAIN HALLE)	46-90					
PHENIA_INCH10	HEMAGGLUTININ-NEURAMINIDASE	MEASLES VIRUS (STRAIN IPJ-CA)	46-87					
PHENIA_INCH11	HEMAGGLUTININ-NEURAMINIDASE	MEASLES VIRUS (STRAIN YAMAGATA-1)	46-87					
PHENIA_INCH12	HEMAGGLUTININ-NEURAMINIDASE	MUMPS VIRUS (STRAIN SBL-1)	34-99					
PHENIA_INCH13	HEMAGGLUTININ-NEURAMINIDASE	MUMPS VIRUS (STRAIN KIVAHARA VACCINE)	34-99					
PHENIA_INCH14	HEMAGGLUTININ-NEURAMINIDASE	MUMPS VIRUS (STRAIN RW)	34-99					
PHENIA_INCH15	HEMAGGLUTININ-NEURAMINIDASE	MUMPS VIRUS (STRAIN SBL)	34-99					
PHENIA_INCH16	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA/072)	471-539					
PHENIA_INCH17	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE C45)	1-49					
PHENIA_INCH18	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN D2476)	1-53					
PHENIA_INCH19	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN MIYADAKI/1)	1-53					
PHENIA_INCH20	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN QUEENSLAND/66)	1-53					
PHENIA_INCH21	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN TEXAS G B/41)	1-49					
PHENIA_INCH22	HEMAGGLUTININ-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN ULSTEIN/3)	1-53					
PHENIA_INCH23	HEMAGGLUTININ-NEURAMINIDASE	PHOCINE DISTEMPER VIRUS	19-73					
PHENIA_INCH24	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN WASHINGTON/1957)	66-110					
PHENIA_INCH25	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 2 VIRUS	247-281					
PHENIA_INCH26	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TOSHIDA)	247-281					
PHENIA_INCH27	HEMAGGLUTININ-NEURAMINIDASE	BOVINE PARAINFLUENZA 3 VIRUS	31-93					
PHENIA_INCH28	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN MH 47853)	13-110					
PHENIA_INCH29	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN AUS/12434/74)	394-428					
PHENIA_INCH30	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TEX/94/590)	394-428					
PHENIA_INCH31	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TEX/95/021)	394-428					
PHENIA_INCH32	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TEX/12637/83)	394-428					
PHENIA_INCH33	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN WASH/04/179)	394-428					
PHENIA_INCH34	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN WASH/13/11/73)	394-428					
PHENIA_INCH35	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIDA)	36-48					
PHENIA_INCH36	HEMAGGLUTININ-NEURAMINIDASE	RACCOON POX VIRUS	66-214					
PHENIA_INCH37	HEMAGGLUTININ-NEURAMINIDASE	RINDERPEST VIRUS (STRAIN KABETE O)	46-87					
PHENIA_INCH38	HEMAGGLUTININ-NEURAMINIDASE	RINDERPEST VIRUS (STRAIN L)	46-87					
PHENIA_INCH39	HEMAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN Z/HOST MUTANTS)	57-110					
PHENIA_INCH40	HEMAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN FUSHIMI)	57-110					
PHENIA_INCH41	HEMAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN HARRIS)	57-110					
PHENIA_INCH42	HEMAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN IIV)	57-110					
PHENIA_INCH43	HEMAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS (STRAIN Z)	57-110					
PHENIA_INCH44	HEMAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS 41	10-52					
PHENIA_INCH45	HEMAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS 5 (STRAIN W3)	37-82					
PHENIA_INCH46	HEMAGGLUTININ-NEURAMINIDASE	SENDAI VIRUS 5 (ISOLATE HUMAN/LN)	37-82					
PHENIA_INCH47	HEMAGGLUTININ-NEURAMINIDASE	VARICELLA VIRUS	177-211					
PHENIA_INCH48	HEMAGGLUTININ PRECURSOR	HUMAN ADENOVIRUS TYPE 2	96-134					
PHENIA_INCH49	PERIPEPTONAL HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH50	PERIPEPTONAL HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH51	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH52	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH53	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH54	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH55	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH56	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH57	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH58	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH59	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH60	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH61	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH62	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH63	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH64	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH65	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH66	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH67	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH68	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH69	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH70	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH71	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH72	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH73	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH74	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH75	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH76	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH77	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH78	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH79	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH80	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH81	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH82	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH83	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH84	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH85	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH86	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH87	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH88	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH89	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH90	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH91	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH92	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH93	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH94	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH95	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH96	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH97	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH98	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH99	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					
PHENIA_INCH100	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 3	96-134					



PCGENE	ALLNOTES	AREAL	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
PROTIN	ALL Viruses (no Bacteriophage)	18-137						
PROTIN	HUMAN ADENOVIRUS TYPE 12	67-126						
PROTIN	HUMAN ADENOVIRUS TYPE 41	53-103						
PROTIN	CANINE ADENOVIRUS TYPE 2	61-109						
PROTIN	TUPAIA ADENOVIRUS	413-467						
PROTIN	HUMAN ADENOVIRUS TYPE 3	320-379						
PROTIN	HUMAN ADENOVIRUS TYPE 40	103-353						
PROTIN	HUMAN ADENOVIRUS TYPE 41	306-355						
PROTIN	HUMAN ADENOVIRUS TYPE 41	301-346						
PROTIN	BOVINE ADENOVIRUS TYPE 3	320-395						
PROTIN	COWPOX VIRUS	110-151						
PROTIN	AFRICAN SWINE FEVER VIRUS (STRAIN BA11V)	1-44						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN BA11)	179-420						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN BA11)	5-37						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CM1111)	178-419						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	1-44						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	5-37						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	178-419						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	5-37						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	178-419						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	5-37						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	178-419						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	5-37						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	178-419						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	5-37						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	178-419						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	5-37						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	178-419						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	5-37						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	178-419						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	5-37						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	178-419						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	5-37						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	178-419						
PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	5-37						
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PROTIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM1)	5-37						
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PCGENE	ALLNOTIS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTEIN	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY1	GENOME POLYPROTEIN 1	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY2	GENOME POLYPROTEIN 2	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY3	GENOME POLYPROTEIN 3	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY4	GENOME POLYPROTEIN 4	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY5	GENOME POLYPROTEIN 5	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY6	GENOME POLYPROTEIN 6	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY7	GENOME POLYPROTEIN 7	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY8	GENOME POLYPROTEIN 8	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY9	GENOME POLYPROTEIN 9	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY10	GENOME POLYPROTEIN 10	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY11	GENOME POLYPROTEIN 11	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY12	GENOME POLYPROTEIN 12	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY13	GENOME POLYPROTEIN 13	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY14	GENOME POLYPROTEIN 14	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY15	GENOME POLYPROTEIN 15	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY16	GENOME POLYPROTEIN 16	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY17	GENOME POLYPROTEIN 17	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY18	GENOME POLYPROTEIN 18	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY19	GENOME POLYPROTEIN 19	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY20	GENOME POLYPROTEIN 20	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY21	GENOME POLYPROTEIN 21	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY22	GENOME POLYPROTEIN 22	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY23	GENOME POLYPROTEIN 23	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY24	GENOME POLYPROTEIN 24	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY25	GENOME POLYPROTEIN 25	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY26	GENOME POLYPROTEIN 26	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY27	GENOME POLYPROTEIN 27	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY28	GENOME POLYPROTEIN 28	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY29	GENOME POLYPROTEIN 29	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY30	GENOME POLYPROTEIN 30	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY31	GENOME POLYPROTEIN 31	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY32	GENOME POLYPROTEIN 32	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY33	GENOME POLYPROTEIN 33	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY34	GENOME POLYPROTEIN 34	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY35	GENOME POLYPROTEIN 35	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY36	GENOME POLYPROTEIN 36	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY37	GENOME POLYPROTEIN 37	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY38	GENOME POLYPROTEIN 38	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY39	GENOME POLYPROTEIN 39	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY40	GENOME POLYPROTEIN 40	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY41	GENOME POLYPROTEIN 41	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY42	GENOME POLYPROTEIN 42	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY43	GENOME POLYPROTEIN 43	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY44	GENOME POLYPROTEIN 44	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY45	GENOME POLYPROTEIN 45	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY46	GENOME POLYPROTEIN 46	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY47	GENOME POLYPROTEIN 47	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY48	GENOME POLYPROTEIN 48	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY49	GENOME POLYPROTEIN 49	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY50	GENOME POLYPROTEIN 50	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY51	GENOME POLYPROTEIN 51	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY52	GENOME POLYPROTEIN 52	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY53	GENOME POLYPROTEIN 53	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY54	GENOME POLYPROTEIN 54	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY55	GENOME POLYPROTEIN 55	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY56	GENOME POLYPROTEIN 56	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY57	GENOME POLYPROTEIN 57	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY58	GENOME POLYPROTEIN 58	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY59	GENOME POLYPROTEIN 59	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY60	GENOME POLYPROTEIN 60	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY61	GENOME POLYPROTEIN 61	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY62	GENOME POLYPROTEIN 62	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY63	GENOME POLYPROTEIN 63	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY64	GENOME POLYPROTEIN 64	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY65	GENOME POLYPROTEIN 65	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY66	GENOME POLYPROTEIN 66	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY67	GENOME POLYPROTEIN 67	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY68	GENOME POLYPROTEIN 68	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY69	GENOME POLYPROTEIN 69	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY70	GENOME POLYPROTEIN 70	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY71	GENOME POLYPROTEIN 71	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY72	GENOME POLYPROTEIN 72	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY73	GENOME POLYPROTEIN 73	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY74	GENOME POLYPROTEIN 74	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY75	GENOME POLYPROTEIN 75	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY76	GENOME POLYPROTEIN 76	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY77	GENOME POLYPROTEIN 77	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY78	GENOME POLYPROTEIN 78	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY79	GENOME POLYPROTEIN 79	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY80	GENOME POLYPROTEIN 80	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY81	GENOME POLYPROTEIN 81	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY82	GENOME POLYPROTEIN 82	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY83	GENOME POLYPROTEIN 83	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY84	GENOME POLYPROTEIN 84	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY85	GENOME POLYPROTEIN 85	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY86	GENOME POLYPROTEIN 86	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY87	GENOME POLYPROTEIN 87	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY88	GENOME POLYPROTEIN 88	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY89	GENOME POLYPROTEIN 89	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY90	GENOME POLYPROTEIN 90	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY91	GENOME POLYPROTEIN 91	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY92	GENOME POLYPROTEIN 92	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY93	GENOME POLYPROTEIN 93	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY94	GENOME POLYPROTEIN 94	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY95	GENOME POLYPROTEIN 95	660-723	724-773	787-818	819-870	871-922	923-974	975-1026	1027-1078
PPOLY96	GENOME POLYPROTEIN 96	660-723	724-77						



[illegible]



PCGENE	ALLNOTES	ALL VITAMIN (see bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
FILE NAME	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PROLO_P013	GENOME POLYPROTEIN	POLIOVIRUS TYPE 2 (STRAIN W-3)	9-43	994-910	1044-099	1412-1448	1408-1546	1607-1648	1805-1819	1901-1946
PROLO_P014	GENOME POLYPROTEIN	POLIOVIRUS TYPE 3 (STRAIN 31127)	9-43	994-910	1044-099	1412-1448	1408-1546	1607-1648	1805-1819	1901-1946
PROLO_P015	GENOME POLYPROTEIN	POLIOVIRUS TYPE 3 (STRAIN 12411B)	9-43	994-910	1044-099	1412-1448	1408-1546	1607-1648	1805-1819	1901-1946
PROLO_P016	GENOME POLYPROTEIN	PLUM POX POLYPROTEIN (STRAIN D)	164-208	441-503	728-769	813-867	921-955	1741-1782		
PROLO_P017	GENOME POLYPROTEIN	PLUM POX POLYPROTEIN (STRAIN EL AMAR)	116-157	784-818	1146-1197					
PROLO_P018	GENOME POLYPROTEIN	PLUM POX POLYPROTEIN (ISOLATE NAT)	164-208	441-503	728-769	813-867	921-955	1741-1782		
PROLO_P019	GENOME POLYPROTEIN	PLUM POX POLYPROTEIN (ISOLATE NAT)	164-208	441-503	728-769	813-867	921-955	1741-1782		
PROLO_P020	GENOME POLYPROTEIN	PAPAYA RINGSPOOT VIRUS (STRAIN P/MUTANT HA)	68-102	434-468						
PROLO_P021	GENOME POLYPROTEIN	PAPAYA RINGSPOOT VIRUS (STRAIN P/MUTANT HA 5-1)	325-359							
PROLO_P022	GENOME POLYPROTEIN	PAPAYA RINGSPOOT VIRUS (STRAIN W)	325-359							
PROLO_P023	GENOME POLYPROTEIN	PEA SEED-BORNE MOSAIC VIRUS (STRAIN DPDI)	253-315	315-389	538-589	931-976	984-1018	1080-1177	1381-1637	1808-1860
PROLO_P024	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN C)	1971-2015	2375-2413	2870-2907					
PROLO_P025	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN HUNGARIAN)	131-196	701-735	802-836	901-949	1401-1441	1492-1526	1728-1772	1777-1818
PROLO_P026	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN M)	144-181	701-735	802-836	901-949	1401-1441	1492-1526	1728-1772	1777-1818
PROLO_P027	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN N)	2272-2306							
PROLO_P028	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN O)	140-196	211-245	701-735	802-836	901-949	1401-1441	1492-1526	1728-1772
PROLO_P029	GENOME POLYPROTEIN	PASSIONFRUIT WOODINESS VIRUS (STRAIN SEVERE)	140-196	211-245	701-735	802-836	901-949	1401-1441	1492-1526	1728-1772
PROLO_P030	GENOME POLYPROTEIN	PASSIONFRUIT WOODINESS VIRUS (STRAIN TIP BRIGHT)	203-237							
PROLO_P031	GENOME POLYPROTEIN	PASSIONFRUIT WOODINESS VIRUS (STRAIN TIP BRIGHT)	203-237							
PROLO_P032	GENOME POLYPROTEIN	PASSIONFRUIT WOODINESS VIRUS (STRAIN TIP BRIGHT)	203-237							
PROLO_P033	GENOME POLYPROTEIN	ST. LOUIS ENCEPHALITIS VIRUS (ISOLATE P-121)	194-228	1111-1172	1378-1413	1858-1899	1950-1991	2703-2737		
PROLO_P034	GENOME POLYPROTEIN	ST. LOUIS ENCEPHALITIS VIRUS (STRAIN MS1-7)	106-143	633-707	729-773	973-1009	1404-1438			
PROLO_P035	GENOME POLYPROTEIN	SWINE VESICULAR DISEASE VIRUS (STRAIN IVO-7)	15-49	1024-1070	1718-1813	1890-1924				
PROLO_P036	GENOME POLYPROTEIN	SWINE VESICULAR DISEASE VIRUS (STRAIN UKG2173)	15-49	1024-1070	1718-1813	1890-1924				
PROLO_P037	GENOME POLYPROTEIN	TICK-BORNE ENCEPHALITIS VIRUS (STRAIN SOE/IN)	68-140	231-272	431-465	1158-1192	1431-1473	1979-1966	2182-2216	2335-2390
PROLO_P038	GENOME POLYPROTEIN	TICK-BORNE ENCEPHALITIS VIRUS (WESTERN SUBTYPE)	2965-2999	3051-3093	3100-3143					
PROLO_P039	GENOME POLYPROTEIN	TICK-BORNE ENCEPHALITIS VIRUS (WESTERN SUBTYPE)	64-140	231-272	431-465	1158-1192	1431-1473	1979-1966	2182-2216	2335-2390
PROLO_P040	GENOME POLYPROTEIN	TOBACCO ETCH VIRUS	3003-3037	3037-3094	3102-3145					
PROLO_P041	GENOME POLYPROTEIN	THEILER'S MURINE ENCEPHALOMYELITIS VIRUS (STRAIN BEAN)	73-124	166-223	540-584	720-782	828-925	1148-1192	1416-1460	1494-1535
PROLO_P042	GENOME POLYPROTEIN	THEILER'S MURINE ENCEPHALOMYELITIS VIRUS (STRAIN BEAN)	1668-1702	1747-1781	1792-1826	2395-2434	2707-2821			
PROLO_P043	GENOME POLYPROTEIN	THEILER'S MURINE ENCEPHALOMYELITIS VIRUS (STRAIN DA)	1306-1340	1483-1518	1601-1635					
PROLO_P044	GENOME POLYPROTEIN	THEILER'S MURINE ENCEPHALOMYELITIS VIRUS (STRAIN GDV)	1306-1340	1483-1518	1601-1635					
PROLO_P045	GENOME POLYPROTEIN	TURNIP MOSAIC VIRUS	216-259	316-363	494-528	768-819	1443-1477			
PROLO_P046	GENOME POLYPROTEIN	TOBACCO VEIN MOTTILING VIRUS	34-48	403-449	647-704	761-813	851-895	949-1017	1031-1072	1643-1677
PROLO_P047	GENOME POLYPROTEIN	WATERMELON MOSAIC VIRUS II	1816-1733	2316-2374	2701-2749	3214-3246				
PROLO_P048	GENOME POLYPROTEIN	WEST NILE VIRUS	68-105	203-236						
PROLO_P049	GENOME POLYPROTEIN	YELLOW FEVER VIRUS (STRAIN 17D)	74-108	303-331	807-881	973-1007	1413-1447	1681-1695	2323-2376	2377-2375
PROLO_P050	GENOME POLYPROTEIN	YELLOW FEVER VIRUS (STRAIN 17D)	3306-3337	3337-3436						
PROLO_P051	GENOME POLYPROTEIN	YELLOW FEVER VIRUS (STRAIN PASTEUR 17D-204)	418-432	535-563	728-748	1388-1444	2321-2376	2477-2565	2938-2994	3097-3143
PROLO_P052	GENOME POLYPROTEIN	YELLOW FEVER VIRUS (STRAIN 119981)	418-432	535-563	728-748	1388-1444	2321-2376	2477-2565	2938-2994	3097-3143
PROLO_P053	GENOME POLYPROTEIN	POLIOVIRUS TYPE 1 (STRAIN MAHONEY)	73-116	418-432	535-563	728-748	1388-1444	2321-2376	2477-2565	2938-2994
PROLO_P054	GENOME POLYPROTEIN	VEZELIAN EQUINE ENCEPHALITIS VIRUS (STRAIN TRINIDAD)	9-43	1007-1102	1413-1449	1591-1349	1610-1651	1808-1842	1904-1949	
PROLO_P055	NON-STRUCTURAL POLYPROTEIN	FELINE CALICIVIRUS (STRAIN CEV48 FIV)	310-344							
PROLO_P056	NON-STRUCTURAL POLYPROTEIN	FELINE CALICIVIRUS (STRAIN FIV)	4-43	369-410	968-1020	1023-1061				
PROLO_P057	NON-STRUCTURAL POLYPROTEIN	HEPATITIS E VIRUS (STRAIN BURMA)	338-379	1139-1177						
PROLO_P058	NON-STRUCTURAL POLYPROTEIN	HEPATITIS E VIRUS (STRAIN MEDCOO)	338-379							
PROLO_P059	NON-STRUCTURAL POLYPROTEIN	HEPATITIS E VIRUS (STRAIN MYANMAR)	338-379							
PROLO_P060	NON-STRUCTURAL POLYPROTEIN	HEPATITIS E VIRUS (STRAIN PAKISTAN)	337-378	1138-1176						
PROLO_P061	NON-STRUCTURAL POLYPROTEIN	MIDDLEBURY VIRUS	922-977							



FIGURE	ALLNOTES	ALL Viruses (see Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PROTEIN	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PROTEIN BUDV	NON-STRUCTURAL POLYPROTEIN	ONYONG-ONYONG VIRUS (STRAIN GULU)	199-973	1942-1986	2444-2502					
PROTEIN BUDV	NON-STRUCTURAL POLYPROTEIN	RABBIT HEMORRHAGIC DISEASE VIRUS	181-234	1857-1716	409-437					
PROTEIN BUDV	NON-STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN NB597)	895-979	1978-1963	2414-2467					
PROTEIN BUDV	NON-STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN T4)	597-431	1803-1136						
PROTEIN BUDV	NON-STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (STRAIN TIENJEN)	1504-1540	1531-1583	1720-1767					
PROTEIN BUDV	NON-STRUCTURAL POLYPROTEIN	SEMURU FOREST VIRUS	1094-1128	2378-2392						
PROTEIN BUDV	NON-STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (SUBTYPE OCKELBO / STRAIN ED5B YN 82-1)	919-971	1491-1535	1941-1996					
PROTEIN BUDV	NON-STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (STRAIN H037)	1491-1535	1941-1535	2442-2478					
PROTEIN BUDV	NON-STRUCTURAL POLYPROTEIN	EGGPLANT MOSAIC VIRUS	899-973	1172-1161						
PROTEIN BUDV	NON-STRUCTURAL POLYPROTEIN	EQUINE ENCEPHALITIS VIRUS	372-406	914-951						
PROTEIN BUDV	NON-STRUCTURAL POLYPROTEIN	EASTERN EQUINE ENCEPHALITIS VIRUS	372-407	914-953						
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	EASTERN EQUINE ENCEPHALITIS VIRUS (STRAIN VASJEN BNC)	1216-1250							
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TC-8)	1216-1250							
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TRINIDAD)	134-168	231-246	470-523					
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	AVIAN INFECTION BURSAL DISEASE VIRUS (STRAIN 2370)	134-168	231-246	470-523					
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	AVIAN INFECTION BURSAL DISEASE VIRUS (STRAIN AUSTRAL)	134-168	231-246	470-523					
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	AVIAN INFECTION BURSAL DISEASE VIRUS (STRAIN CU-1)	134-168	231-246	470-523					
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	AVIAN INFECTION BURSAL DISEASE VIRUS (STRAIN E)	134-168	231-246	470-523					
PROTEIN BUDV	NON-STRUCTURAL POLYPROTEIN	AVIAN INFECTION BURSAL DISEASE VIRUS (STRAIN P80-98)	113-149	212-287	451-504					
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	AVIAN INFECTION BURSAL DISEASE VIRUS (STRAIN STC)	134-168	249-283	470-523					
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	AVIAN INFECTION BURSAL DISEASE VIRUS (SUBTYPE JASPER)	69-103	723-785						
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	INFECTION PANCREATIC NECROSIS VIRUS (STRAIN NI)	716-746							
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	ONYONG-ONYONG VIRUS (STRAIN GULU)	1204-1238							
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN 211970)	35-49							
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN NB597)	369-403	938-973						
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	ROSS RIVER VIRUS (STRAIN T4)	938-973							
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (VACCINE STRAIN HP77)	999-1036							
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (VACCINE STRAIN R4370)	999-1036							
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (STRAIN TIENJEN)	999-1036							
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (SUBTYPE OCKELBO / STRAIN ED5B YN 82-1)	162-396							
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (STRAINS HRP AND HOLY)	162-396							
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (WILD TYPE S8 DERIVED FROM STRAIN AU39)	34-68							
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	WESTERN EQUINE ENCEPHALITIS VIRUS	913-947							
PROTEIN BUDV	STRUCTURAL POLYPROTEIN	SABON ENDORGENOUS VIRUS (STRAIN M7)	42-80	676-743	794-823	1001-1042				
PROTEIN BUDV	POL POLYPROTEIN	BOVINE LEUKEMIA VIRUS (AUSTRALIAN ISOLATE)	623-473							
PROTEIN BUDV	POL POLYPROTEIN	BOVINE LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1)	623-473							
PROTEIN BUDV	POL POLYPROTEIN	CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (STRAIN COME)	179-214							
PROTEIN BUDV	POL POLYPROTEIN	CALIFLOWER MOSAIC VIRUS (STRAIN DM)	177-211							
PROTEIN BUDV	ENZYMATIC POLYPROTEIN	COMPELINA YELLOW MOTTLE VIRUS	87-121	333-367	417-499	1010-1231				
PROTEIN BUDV	PUTATIVE POLYPROTEIN	EQUINE INFECTION ANEMIA VIRUS (CLONE 1349)	513-566	1023-1034						
PROTEIN BUDV	POL POLYPROTEIN	EQUINE INFECTION ANEMIA VIRUS (CLONE C13)	513-566	1023-1034						
PROTEIN BUDV	POL POLYPROTEIN	EQUINE INFECTION ANEMIA VIRUS (ISOLATE WYOMING)	513-565	1021-1035						
PROTEIN BUDV	POL POLYPROTEIN	FELINE ENDOGENOUS VIRUS ECEI	533-600	623-439	815-899					
PROTEIN BUDV	POL POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUMA)	439-473	604-603						
PROTEIN BUDV	POL POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	438-472	606-642						
PROTEIN BUDV	POL POLYPROTEIN	FELINE IMMUNODEFICIENCY VIRUS (ISOLATE TAC)	438-472	593-642						
PROTEIN BUDV	POL POLYPROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DX3)	403-417							
PROTEIN BUDV	ENZYMATIC POLYPROTEIN	HUMAN SPUMONETROVIRUS (FOAMY VIRUS)	140-174	217-254	283-326					
PROTEIN BUDV	POL POLYPROTEIN	GIBBON APE LEUKEMIA VIRUS	528-562	678-711						
PROTEIN BUDV	POL POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE 1 (STRAIN ATL)	678-711							
PROTEIN BUDV	POL POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE 1 (CARIBBEAN ISOLATE)	678-711							
PROTEIN BUDV	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ARV25F7 ISOLATE)	501-537	604-664						
PROTEIN BUDV	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RH10 ISOLATE)	513-549	639-676						



PGCENE	ALL MOTIS	FILE NAME	FILE NAME	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PPOL_HV1A	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (HIS ISOLATE)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (HIS ISOLATE)	513-349	513-349	513-349	513-349	513-349	513-349	513-349	513-349
PPOL_HV1B	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (BRU ISOLATE)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (BRU ISOLATE)	513-349	513-349	513-349	513-349	513-349	513-349	513-349	513-349
PPOL_HV1C	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (ELJ ISOLATE)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (ELJ ISOLATE)	500-336	500-336	500-336	500-336	500-336	500-336	500-336	500-336
PPOL_HV1D	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (HXB3 ISOLATE)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (HXB3 ISOLATE)	501-337	501-337	501-337	501-337	501-337	501-337	501-337	501-337
PPOL_HV1E	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (JRC5F ISOLATE)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (JRC5F ISOLATE)	501-341	501-341	501-341	501-341	501-341	501-341	501-341	501-341
PPOL_HV1F	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (JAL ISOLATE)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (JAL ISOLATE)	476-336	476-336	476-336	476-336	476-336	476-336	476-336	476-336
PPOL_HV1G	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (JAL ISOLATE)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (JAL ISOLATE)	504-340	504-340	504-340	504-340	504-340	504-340	504-340	504-340
PPOL_HV1H	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (NEW YORK-3 ISOL)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (NEW YORK-3 ISOL)	501-337	501-337	501-337	501-337	501-337	501-337	501-337	501-337
PPOL_HV1I	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE)	500-336	500-336	500-336	500-336	500-336	500-336	500-336	500-336
PPOL_HV1J	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (OY1 ISOLATE)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (OY1 ISOLATE)	501-337	501-337	501-337	501-337	501-337	501-337	501-337	501-337
PPOL_HV1K	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (PV22 ISOLATE)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (PV22 ISOLATE)	513-349	513-349	513-349	513-349	513-349	513-349	513-349	513-349
PPOL_HV1L	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (R/HAT ISOLATE)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (R/HAT ISOLATE)	500-336	500-336	500-336	500-336	500-336	500-336	500-336	500-336
PPOL_HV1M	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (STRAIN UGANDAN)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (STRAIN UGANDAN)	500-336	500-336	500-336	500-336	500-336	500-336	500-336	500-336
PPOL_HV1N	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (23/CDC-234 ISOLA	HUMAN DAKUNODEFICIENCY VIRUS TYPE 1 (23/CDC-234 ISOLA	500-336	500-336	500-336	500-336	500-336	500-336	500-336	500-336
PPOL_HV1O	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE BEM)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE BEM)	484-382	484-382	484-382	484-382	484-382	484-382	484-382	484-382
PPOL_HV1P	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE C4M)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE C4M)	516-390	516-390	516-390	516-390	516-390	516-390	516-390	516-390
PPOL_HV1Q	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D1M)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D1M)	502-400	502-400	502-400	502-400	502-400	502-400	502-400	502-400
PPOL_HV1R	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D2M)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D2M)	516-410	516-410	516-410	516-410	516-410	516-410	516-410	516-410
PPOL_HV1S	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE GHANA-1)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE GHANA-1)	464-362	464-362	464-362	464-362	464-362	464-362	464-362	464-362
PPOL_HV1T	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE NHI-2)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE NHI-2)	44-78	44-78	44-78	44-78	44-78	44-78	44-78	44-78
PPOL_HV1U	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	357-391	357-391	357-391	357-391	357-391	357-391	357-391	357-391
PPOL_HV1V	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SBLIS1)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SBLIS1)	46-40	46-40	46-40	46-40	46-40	46-40	46-40	46-40
PPOL_HV1W	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	484-318	484-318	484-318	484-318	484-318	484-318	484-318	484-318
PPOL_HV1X	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	462-503	462-503	462-503	462-503	462-503	462-503	462-503	462-503
PPOL_HV1Y	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	190-231	190-231	190-231	190-231	190-231	190-231	190-231	190-231
PPOL_HV1Z	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	322-392	322-392	322-392	322-392	322-392	322-392	322-392	322-392
PPOL_HV2A	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2B	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	482-749	482-749	482-749	482-749	482-749	482-749	482-749	482-749
PPOL_HV2C	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	682-749	682-749	682-749	682-749	682-749	682-749	682-749	682-749
PPOL_HV2D	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	682-749	682-749	682-749	682-749	682-749	682-749	682-749	682-749
PPOL_HV2E	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2F	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2G	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2H	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2I	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2J	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2K	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2L	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2M	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2N	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2O	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2P	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2Q	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2R	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2S	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2T	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2U	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2V	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2W	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2X	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2Y	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV2Z	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3A	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3B	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3C	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3D	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3E	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3F	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3G	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3H	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3I	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3J	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3K	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3L	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3M	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3N	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3O	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3P	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3Q	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3R	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3S	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	672-744	672-744	672-744	672-744	672-744
PPOL_HV3T	POL POLYPROTEIN	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	HUMAN DAKUNODEFICIENCY VIRUS TYPE 2 (ISOLATE 37)	672-744	672-744	672-744	67				



[illegible]



PGCENE	ALLANOTIS	All Virus (no bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
PROTEIN	RUBINUS	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	032-468							
PUR1, HSVB	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)		76-110							
PUR1, HSVB	HERPESVIRUS SAIMIRI (STRAIN II)		324-365							
PUR1, VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)		167-402							
PUR1, VACC	VACCINIA VIRUS (STRAIN WR)		367-402							
PUR1, VACC	VARIOLA VIRUS		367-402							
PUR1, ZVD	MARICELLA-ZOSTER VIRUS (STRAIN DUINAS)		223-337							
PUR1, EBY	EPSTEIN-BARR VIRUS (STRAIN B95-4)		89-137							
PUR1, HSVB	BOVINE HERPESVIRUS TYPE 1 (STRAIN 34)		101-135							
PUR1, HSVB	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)		106-140							
PUR1, SVKKA	HERPESVIRUS SAIMIRI (STRAIN I)		123-159							
PUR1, VACC	SHOPE FIBROBLAST VIRUS (STRAIN KASZA)		98-132							
PUR1, VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)		98-132							
PUR1, VACC	VACCINIA VIRUS (STRAIN L-IVP)		98-132							
PUR1, VARV	VACCINIA VIRUS (STRAIN WR)		98-132							
PUR1, HSVH	VARIOLA VIRUS		98-132							
PUR1, VACC	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG51)		171-212							
PUR1, VACC	VACCINIA VIRUS (STRAIN WR) AND (STRAIN COPENHAGEN)		118-150							
PUR1, VACC	VARIOLA VIRUS		41-73							
PUR1, VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)		243-291							
PUR1, VACC	VACCINIA VIRUS (STRAIN WR)		243-291							
PUR1, CAPVK	VARIOLA VIRUS		243-291							
PUR1, COMPX	CAPPOXYRICKS (STRAIN KS-1)		19-400							
PUR1, VACC	COMPOX VIRUS		211-245							
PUR1, VARV	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPENHAGEN)		211-245							
PUR1, VACC	VARIOLA VIRUS		211-245							
PUR1, VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)		63-116							
PUR1, VACC	VARIOLA VIRUS		63-116							
PUR1, VACC	VACCINIA VIRUS (STRAIN COPENHAGEN)		1-71							
PUR1, VARV	VACCINIA VIRUS (STRAIN WR)		1-71							
PUR1, VACC	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPENHAGEN)		23-59							
PUR1, VARV	VARIOLA VIRUS		23-59							
PUR1, VACC	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPENHAGEN)		43-93							
PUR1, VARV	VARIOLA VIRUS		43-93							
PUR1, LEFV	LELYSTAD VIRUS		1533-1567							
PUR1, MANN	EQUINE ARTERITIS VIRUS		1721-1758							
PUR1, LABEL	INFLUENZA A VIRUS (STRAIN ANANN ARBOR/6460)		1003-1117							
PUR1, JAGUN	INFLUENZA A VIRUS (STRAIN AREQUIPA/1156)		171-242							
PUR1, JAGUN	INFLUENZA A VIRUS (STRAIN AGOUNEDJIN/471)		171-242							
PUR1, JAGUN	INFLUENZA A VIRUS (STRAIN ACULUMARYLAND/70477)		171-242							
PUR1, JAHLO	INFLUENZA A VIRUS (STRAIN MEQUENZLONDAVI/11973)		160-242							
PUR1, JAITE	INFLUENZA A VIRUS (STRAIN AREQUINETENNESSEE/496)		160-242							
PUR1, JAKIE	INFLUENZA A VIRUS (STRAIN AKLEY/19377)		171-242							
PUR1, JAKOR	INFLUENZA A VIRUS (STRAIN AKOREJA/2166)		171-242							
PUR1, LAJEI	INFLUENZA A VIRUS (STRAIN ALENDINGRADY/1462)		171-242							
PUR1, LAE2	INFLUENZA A VIRUS (STRAIN ALENDINGRADY/1462737)		171-242							
PUR1, LALES	INFLUENZA A VIRUS (STRAIN AMALLARDNEW YORK/473071)		171-242							
PUR1, LANAM	INFLUENZA A VIRUS (STRAIN AMEDAPHIS/5048)		171-242							
PUR1, JANES	INFLUENZA A VIRUS (STRAIN AMEDAPHIS/5048)		171-242							
PUR1, JANIS	INFLUENZA A VIRUS (STRAIN AMEDAPHIS/5048)		171-242							
PUR1, JANIS	INFLUENZA A VIRUS (STRAIN AMEDAPHIS/5048)		171-242							



[illegible]



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PGC#	ALL MOTIS	Ad Virus (no bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
FILE NAME	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PRAPL_SEQU	RNA POLYMERASE BETA SUBUNIT	SENDAL VIRUS (STRAIN 2)	2146-2216	540-600	617-656	747-781	1064-1119	1239-1280	1699-1736	2000-2034
PRAPL_SVIR	RNA-DIRECTED RNA POLYMERASE	SEUL VIRUS (STRAIN 80-19)	98-139	174-204	357-591	635-696	721-763	1742-1776	1947-1981	1991-2027
PRAPL_STNY	RNA POLYMERASE BETA SUBUNIT	SDAGAN VIRUS 5 (STRAIN 21004-WK)	547-627	742-781	1235-1280	1310-1353	1592-1626	1676-1715	2024-2058	
PRAPL_TNYV	RNA POLYMERASE BETA SUBUNIT	SOMORUS YELLOW NET VIRUS	760-794	925-939	977-1014	1089-1137	1178-1202	2039-2107		
PRAPL_UK	RNA-DIRECTED RNA POLYMERASE	TOMATO SPOTTED WILT VIRUS (BRAZILIAN ISOLATE CPN/10/8)	44-101	399-433	519-573	589-634	1119-1152	1195-1236	1321-1379	1538-1572
		UKUNIBEMI VIRUS	1884-1723	1837-1894	2073-2127	2156-2200	2266-2247	2315-2368	2378-2419	2809-2843
PRAPL_VSVH	RNA POLYMERASE	VELOCULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRA)	127-183	212-223	816-874	1030-1071	1481-1513	2015-2049	2061-2098	
PRAPL_VYDV	RNA POLYMERASE BETA SUBUNIT	VELOCULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRA)	319-358	674-715	720-763	1522-1567	1802-1836			
PRAPL_VYSE	RNA POLYMERASE BETA SUBUNIT	VELOCULAR STOMATITIS VIRUS (SEROTYPE SAN JUAN)	319-358	674-715	720-763	1522-1567	1802-1836			
PRAPL_ACLS	RNA POLYMERASE BETA SUBUNIT	VELOCULAR STOMATITIS VIRUS (ISOLATE FL-1)	228-262	357-396	916-950	1235-1269				
PRAPL_BWTV	PUTATIVE RNA-DIRECTED RNA POLYMERASE	APPLE CHLOROTIC LEAF SPOT VIRUS	304-341							
PRAPL_BVDV	PUTATIVE RNA-DIRECTED RNA POLYMERASE	BEET WESTERN YELLOW VIRUS (ISOLATE FL-1)	334-385							
PRAPL_BVDV	PUTATIVE RNA-DIRECTED RNA POLYMERASE	BARLEY YELLOW DWARF VIRUS (ISOLATE MAV-PS1)	234-285							
PRAPL_BVDV	PUTATIVE RNA-DIRECTED RNA POLYMERASE	BARLEY YELLOW DWARF VIRUS (ISOLATE PAV)	234-285							
PRAPL_CADV	PUTATIVE RNA-DIRECTED RNA POLYMERASE	BARLEY YELLOW DWARF VIRUS (ISOLATE P-PAV)	91-131							
PRAPL_CGAV	PROBABLE RNA-DIRECTED RNA POLYMERASE	CARNATION MOTTLE VIRUS	7-41	387-428	446-480	716-763	1445-1479			
PRAPL_DDV1	PUTATIVE RNA-DIRECTED RNA POLYMERASE	CUCUMBER GREEN MOTTLE MOSAIC VIRUS (WATERGELON STR)	316-432	446-484						
PRAPL_DDV2	PUTATIVE RNA-DIRECTED RNA POLYMERASE	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN AUSTRAL)	144-183	266-307	709-757	771-809				
PRAPL_DDV3	PUTATIVE RNA-DIRECTED RNA POLYMERASE	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN AUSTRAL)	147-181	268-307	501-535	710-802				
PRAPL_DDV4	PUTATIVE RNA-DIRECTED RNA POLYMERASE	INFECTIOUS PANCREATIC NECROSIS VIRUS (SEROTYPE JASPER)	147-181	268-307	501-535	710-802				
PRAPL_DDV5	PUTATIVE RNA-DIRECTED RNA POLYMERASE	INFECTIOUS PANCREATIC NECROSIS VIRUS (SEROTYPE SP)	201-246	805-846	936-960	1309-1343	2090-2124			
PRAPL_DDV6	PUTATIVE RNA-DIRECTED RNA POLYMERASE	LYMPHOCTIC CHORIOENCEPHALITIS VIRUS (STRAIN WE)	301-345	697-731						
PRAPL_DDV7	PUTATIVE RNA-DIRECTED RNA POLYMERASE	LYMPHOCTIC CHORIOENCEPHALITIS VIRUS (STRAIN WE)	181-215	697-731						
PRAPL_DDV8	PROBABLE RNA-DIRECTED RNA POLYMERASE	MAIZE CHLOROTIC MOTTLE VIRUS	221-258							
PRAPL_DDV9	PUTATIVE RNA-DIRECTED RNA POLYMERASE	PEA ENATION MOSAIC VIRUS	316-373	471-457						
PRAPL_DDV10	PUTATIVE RNA-DIRECTED RNA POLYMERASE	POTATO LEAFROLL VIRUS (STRAIN 1)	316-373	471-457						
PRAPL_DDV11	PUTATIVE RNA-DIRECTED RNA POLYMERASE	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	316-373	471-457						
PRAPL_DDV12	PUTATIVE RNA-DIRECTED RNA POLYMERASE	PEPPER MILD MOTTLE VIRUS (STRAIN SPAIN)	316-373	471-457						
PRAPL_DDV13	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	666-700							
PRAPL_DDV14	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV15	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV16	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV17	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV18	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV19	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV20	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV21	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV22	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV23	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV24	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV25	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV26	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV27	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV28	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV29	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV30	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV31	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV32	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV33	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV34	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV35	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV36	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV37	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV38	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV39	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV40	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV41	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV42	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV43	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV44	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV45	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV46	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV47	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV48	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV49	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV50	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV51	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV52	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV53	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV54	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV55	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV56	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV57	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV58	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV59	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV60	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV61	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV62	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV63	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV64	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV65	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV66	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV67	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV68	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV69	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV70	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV71	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV72	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV73	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV74	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV75	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV76	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV77	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV78	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV79	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV80	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV81	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV82	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV83	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV84	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV85	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV86	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV87	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV88	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV89	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV90	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV91	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV92	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV93	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV94	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV95	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV96	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV97	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV98	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV99	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							
PRAPL_DDV100	PUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIRUS	310-361							



PCGENE	ALLMOTIS	ALL VIRUSES (see bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
FILE NAME	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PRPP_BA1A	RNA-DIRECTED RNA POLYMERASE	TORACCO NECROSIS VIRUS (STRAIN D)	102-144							
PRPP_CDVO	RNA POLYMERASE ALPHA SUBUNIT	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A11901)	99-158		160-216					
PRPP_HRSV	RNA POLYMERASE ALPHA SUBUNIT	CANINE DISTEMPER VIRUS (STRAIN ORDERSTPOORT)	313-373							
PRPP_HRSV1	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS	99-158		160-216					
PRPP_HRSV2	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN A2)	99-158		160-216					
PRPP_MEAS	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP A / STRAIN A1)	99-158		160-216					
PRPP_MEAS1	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN EDMONSTON)	315-374		460-495					
PRPP_MEAS2	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN IP-3-CA)	315-374		460-495					
PRPP_MUMPS	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN YAMAGATA-1)	315-374		460-495					
PRPP_MUMPS1	RNA POLYMERASE ALPHA SUBUNIT	MUMPS VIRUS (STRAIN SBL-1)	149-183		213-375					
PRPP_MUMPS2	RNA POLYMERASE ALPHA SUBUNIT	MUMPS VIRUS (STRAIN ENDERS)	214-376							
PRPP_MUMPS3	RNA POLYMERASE ALPHA SUBUNIT	MUMPS VIRUS (STRAIN MUYAHARA VACCINE)	214-376							
PRPP_MUMPS4	RNA POLYMERASE ALPHA SUBUNIT	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA/02)	100-134							
PRPP_MUMPS5	RNA POLYMERASE ALPHA SUBUNIT	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE C/45)	100-134							
PRPP_P11HC	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C13)	80-114		313-364					
PRPP_P11HD	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C19)	80-114		313-364					
PRPP_P11HE	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C1-37/1)	80-114		313-364					
PRPP_P11H	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C1-14/130)	86-114		217-371					
PRPP_P11H1	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS	215-381							
PRPP_P11H2	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIBA)	215-381							
PRPP_P11H3	RNA POLYMERASE ALPHA SUBUNIT	BOVINE PARAINFLUENZA 3 VIRUS	31-130		414-470					
PRPP_P11H4	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 41815)	410-599							
PRPP_P11H5	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIBA)	4-38		222-285					
PRPP_P11H6	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 4B VIRUS (STRAIN 68-322)	222-285							
PRPP_P11H7	RNA POLYMERASE ALPHA SUBUNIT	P11 VIRUS	137-174							
PRPP_P11H8	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN A VOI)	93-127							
PRPP_P11H9	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN CVS-11)	93-127							
PRPP_P11H10	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN ERA), AND (STRAIN PM)	93-127							
PRPP_P11H11	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN PV)	93-127							
PRPP_P11H12	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN SAD B19)	93-127							
PRPP_P11H13	RNA POLYMERASE ALPHA SUBUNIT	SENDAL VIRUS (STRAIN 2 / HOST MUTANTS)	313-364		375-447					
PRPP_P11H14	RNA POLYMERASE ALPHA SUBUNIT	SENDAL VIRUS (STRAIN 694)	323-364		375-447					
PRPP_P11H15	RNA POLYMERASE ALPHA SUBUNIT	SENDAL VIRUS (STRAIN FUSHING)	313-364		375-447					
PRPP_P11H16	RNA POLYMERASE ALPHA SUBUNIT	SENDAL VIRUS (STRAIN HARRIS)	313-364		375-447					
PRPP_P11H17	RNA POLYMERASE ALPHA SUBUNIT	SENDAL VIRUS (STRAIN 2)	313-364		375-447					
PRPP_P11H18	RNA POLYMERASE ALPHA SUBUNIT	SENDAL VIRUS 3 (STRAIN W3)	205-278							
PRPP_P11H19	RNA POLYMERASE ALPHA SUBUNIT	SONCHUS YELLOW NET VIRUS	138-173		231-381					
PRPP_P11H20	RNA POLYMERASE ALPHA SUBUNIT	VEESICULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN C1-43)	1-43							
PRPP_P11H21	RNA POLYMERASE ALPHA SUBUNIT	VEESICULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN M1-43)	1-43							
PRPP_P11H22	RNA POLYMERASE ALPHA SUBUNIT	VEESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN 1-37)	1-37							
PRPP_P11H23	RNA POLYMERASE ALPHA SUBUNIT	VEESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN 1-43)	1-43							
PRPP_P11H24	RNA POLYMERASE ALPHA SUBUNIT	VEESICULAR STOMATITIS VIRUS (STRAIN SAN JUAN)	223-264		361-393					
PRPP_P11H25	RNA POLYMERASE ALPHA SUBUNIT	AMERICAN MOORE ENTOMOPHAGUS VIRUS	223-264		361-393					
PRPP_P11H26	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WR)	21-46							
PRPP_P11H27	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS	21-46							
PRPP_P11H28	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN COPENHAGEN)	118-167		221-266					
PRPP_P11H29	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WR)	118-167		221-266					



[illegible]



PCGENE	ALLNOTES	AB Virus (not bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
P10N_A151	DNA TERMINAL PROTEIN	HUMAN ADENOVIRUS TYPE 12	403-491	491-531					
P10N_A154	TRANSFORMING PROTEIN RUN	AVIAN SARCOMA VIRUS (STRAIN 17)	210-264						
P10P_3FVLA	TRANSFORMING PROTEIN MAF	AVIAN MUSCULOPHOSPHATE FIBROSARCOMA VIRUS AS43	207-288	291-340					
P10P_4SFB7	DNA TOPOISOMERASE II	SHORE FIBROMA VIRUS (STRAIN KASZA)	127-183	289-310					
P10P_4SPM4	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (STRAIN BATTIV)	146-180	481-515	601-643	1031-1093	1123-1162		
P15S_5H4AV	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (ISOLATE MALAWI LIL 20/1)	146-180	480-514	600-641	944-978	1031-1091	1123-1161	
P15Y_VZVD	POD-RELATED TRANSFORMING PROTEIN P18-515	SHAGAN SARCOMA VIRUS	16-71						
PUBIL_NPVP	THYMIDYLATE SYNTHASE	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	215-260						
PUL01_HCMVA	UBIQUITIN-LIKE PROTEIN	ORGYIA PSEUDOTISIGATA MULTICAPSID POLYHEDROUS VIRUS	41-80						
PUL01_HSV11	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	169-203						
PUL01_HSV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	94-128						
PUL01_HSV2H	PROTEIN UL3	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN HG33)	92-126						
PUL04_HSV11	GENE 60 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	70-104						
PUL04_HSV11	PROTEIN UL4	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	102-136						
PUL04_HSV11	PROTEIN BBAF1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	104-145	313-347	378-410				
PUL04_HSV11	HYPOTHETICAL PROTEIN UL4	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	216-250						
PUL04_HSV2B	VIRION PROTEIN UL6	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	36-94	107-141	294-329	337-371	416-479		
PUL04_HSV3A	VIRION GENE 36 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	62-170	337-411	448-503				
PUL04_VZVD	VIRION GENE 41 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	90-140	131-194	302-338	364-403			
PUL08_HCMVA	VIRION GENE 34 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	87-131	330-409	704-738				
PUL09_HSV2B	HYPOTHETICAL PROTEIN UL3	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-30						
PUL09_HSV2B	ORIGIN OF REPLICATION BINDING PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	174-208						
PUL11_HCMVA	ORIGIN OF REPLICATION BINDING PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	122-163						
PUL11_HCMVA	NONSENSE								
PUL14_HCMVA	HYPOTHETICAL PROTEIN UL11	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	47-81	185-227					
PUL14_HSV2B	HYPOTHETICAL PROTEIN UL14	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	103-143						
PUL14_HSV2B	HYPOTHETICAL GENE 48 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	32-96	246-283					
PUL14_VZVD	UL14 PROTEIN HOMOLOG	PSEUDORABIES VIRUS (STRAIN MA-3)	43-85						
PUL16_HSV2B	HYPOTHETICAL GENE 46 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	81-103						
PUL17_HSV6U	GENE 48 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	366-390						
PUL31_HSV2B	PROTEIN IOR	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	235-380						
PUL31_HSV2B	GENE 46 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	44-78	421-474					
PUL34_HCMVA	HYPOTHETICAL PROTEIN UL23	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	217-253						
PUL34_HSV2T	HYPOTHETICAL PROTEIN UL34	INFECTION LARYNGOTRACHEITIS VIRUS (STRAIN THORNE VIR)	5-39						
PUL35_HCMVA	HYPOTHETICAL PROTEIN UL35	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	161-195						
PUL35_HSV2B	VIRION PROTEIN UL25	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	333-341	331-399					
PUL35_HSV3A	VIRION GENE 19 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	370-411						
PUL35_HSV3A	VIRION GENE 23 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	364-413						
PUL35_HSV3A	VIRION GENE 19 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	39-92	183-221	363-406				
PUL35_VZVD	64.1 KD VIRION PROTEIN	INFECTION LARYNGOTRACHEITIS VIRUS (STRAIN THORNE VIR)	38-84	163-206					
PUL37_HCMVA	PROBABLE MAJOR ENVELOPE GLYCOPROTEIN 28	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	246-283						
PUL37_HSV2B	PROBABLE MAJOR ENVELOPE GLYCOPROTEIN 28	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	151-187						
PUL31_VZVD	HYPOTHETICAL PROTEIN UL31	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	183-197						
PUL32_HSV2B	GENE 27 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	342-376						
PUL32_HSV2B	MAJOR ENVELOPE GLYCOPROTEIN 300	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	72-106	396-444					
PUL33_HCMVA	PROBABLE MAJOR ENVELOPE GLYCOPROTEIN 28	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	94-133	309-352					
PUL33_VZVD	G-PROTEIN COUPLED RECEPTOR HOMOLOG UL33	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	29-43						
PUL34_HSV11	GENE 23 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	119-200						
PUL34_HSV11	BPFL1 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	113-147						
PUL35_HCMVA	HYPOTHETICAL PROTEIN UL34	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	187-231						
PUL35_HSV2B	VIRION PROTEIN UL34	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	231-268						
PUL37_HSV11	HYPOTHETICAL PROTEIN UL35	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)							



PCGENE	ALLIOTIS	All Viruses (see Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PROTEIN	PROTEIN	HERPESVIRUS (STRAIN B91-4)	701-742							
PROTEIN BOLF1	PROTEIN BOLF1	HERPESVIRUS (STRAIN B91-4)	701-742							
PROTEIN UL37	PROTEIN UL37	HERPESVIRUS TYPE 1 (STRAIN AD4P)	82-137	311-345	614-648	713-750	781-822			
GENE 31 PROTEIN	GENE 31 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	6-63	682-741						
GENE 61 PROTEIN	GENE 61 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	715-753	786-827						
GENE 31 PROTEIN	GENE 31 PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	10-31							
HYPOTHETICAL PROTEIN UL38	HYPOTHETICAL PROTEIN UL38	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	330-364							
HOST SHUTOFF VIRION PROTEIN	HOST SHUTOFF VIRION PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	334-364	321-363						
DNA-BINDING PROTEIN UL41	DNA-BINDING PROTEIN UL41	HERPESVIRUS TYPE 1 (STRAIN AD4P)	138-172							
DNA-BINDING GENE 18 PROTEIN	DNA-BINDING GENE 18 PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	32-109							
HYPOTHETICAL PROTEIN UL43	HYPOTHETICAL PROTEIN UL43	EQUINE HERPESVIRUS TYPE 4 (STRAIN AD4P)	37-48							
MEMBRANE PROTEIN UL43 HOMOLOG	MEMBRANE PROTEIN UL43 HOMOLOG	HERPESVIRUS TYPE 1 (STRAIN AD4P)	312-363							
GENE 11 MEMBRANE PROTEIN	GENE 11 MEMBRANE PROTEIN	HERPESVIRUS TYPE 1 (STRAIN AD4P)	96-137							
PROTEIN UL43	PROTEIN UL43	HERPESVIRUS TYPE 1 (STRAIN AD4P)	96-137							
PROTEIN UL47	PROTEIN UL47	HERPESVIRUS TYPE 1 (STRAIN AD4P)	114-161	745-816						
VIRION PROTEIN UL47	VIRION PROTEIN UL47	HERPESVIRUS TYPE 1 (STRAIN AD4P)	473-511							
60.7 KD ALPHA TRANS-INDUCING PROTEIN	60.7 KD ALPHA TRANS-INDUCING PROTEIN	HERPESVIRUS TYPE 1 (STRAIN AD4P)	561-612							
97 KD ALPHA TRANS-INDUCING PROTEIN	97 KD ALPHA TRANS-INDUCING PROTEIN	HERPESVIRUS TYPE 1 (STRAIN AD4P)	182-248	821-866						
97 KD ALPHA TRANS-INDUCING PROTEIN	97 KD ALPHA TRANS-INDUCING PROTEIN	HERPESVIRUS TYPE 1 (STRAIN AD4P)	219-253	817-866						
ALPHA TRANS-INDUCING FACTOR 91.8 KD PROTEIN	ALPHA TRANS-INDUCING FACTOR 91.8 KD PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	84-135	156-209	664-701					
PROTEIN UL39	PROTEIN UL39	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	153-189							
PROTEIN UL31	PROTEIN UL31	HERPESVIRUS TYPE 1 (STRAIN AD4P)	118-169							
GENE 8 PROTEIN	GENE 8 PROTEIN	HERPESVIRUS TYPE 4 (STRAIN AD42)	121-162							
GENE 8 PROTEIN	GENE 8 PROTEIN	HERPESVIRUS TYPE 1 (STRAIN AD4P)	120-161							
GENE 7 PROTEIN	GENE 7 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	122-163							
PROBABLE DNA REPLICATION PROTEIN BSLF1	PROBABLE DNA REPLICATION PROTEIN BSLF1	HERPESVIRUS (STRAIN B91-4)	188-235							
DNA REPLICATION PROTEIN UL31	DNA REPLICATION PROTEIN UL31	HERPESVIRUS TYPE 1 (STRAIN AD4P)	189-232							
DNA REPLICATION PROTEIN UL33	DNA REPLICATION PROTEIN UL33	HERPESVIRUS TYPE 1 (STRAIN AD4P)	141-182	929-970						
PROBABLE DNA REPLICATION GENE 36 PROTEIN	PROBABLE DNA REPLICATION GENE 36 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	441-481							
PROBABLE DNA REPLICATION GENE 6 PROTEIN	PROBABLE DNA REPLICATION GENE 6 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	201-242							
PROTEIN UL33	PROTEIN UL33	HERPESVIRUS SAIMIRI (STRAIN 11)	12-48							
HYPOTHETICAL PROTEIN UL44	HYPOTHETICAL PROTEIN UL44	HERPESVIRUS TYPE 2 (STRAIN HG33)	131-153							
PROBABLE DNA REPLICATION PROTEIN UL36	PROBABLE DNA REPLICATION PROTEIN UL36	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	32-31							
PROBABLE DNA REPLICATION PROTEIN UL36	PROBABLE DNA REPLICATION PROTEIN UL36	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	39-59							
HYPOTHETICAL PROTEIN UL36	HYPOTHETICAL PROTEIN UL36	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	41-79							
HYPOTHETICAL PROTEIN UL36	HYPOTHETICAL PROTEIN UL36	HERPESVIRUS TYPE 6 (STRAIN UGANDA-1102)	229-270							
HYPOTHETICAL GENE 34 PROTEIN	HYPOTHETICAL GENE 34 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	366-400	512-616						
HYPOTHETICAL GENE 39 PROTEIN	HYPOTHETICAL GENE 39 PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	312-391							
HYPOTHETICAL GENE 39 PROTEIN	HYPOTHETICAL GENE 39 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	24-38							
HYPOTHETICAL GENE 39 PROTEIN	HYPOTHETICAL GENE 39 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	107-144							
HYPOTHETICAL GENE 39 PROTEIN	HYPOTHETICAL GENE 39 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	79-118							
HYPOTHETICAL PROTEIN UL92	HYPOTHETICAL PROTEIN UL92	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	101-143							
HYPOTHETICAL PROTEIN UL92	HYPOTHETICAL PROTEIN UL92	HERPESVIRUS TYPE 6 (STRAIN UGANDA-1102)	18-122							
HYPOTHETICAL GENE 31 PROTEIN	HYPOTHETICAL GENE 31 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	32-37	399-384						
PROTEIN UL93	PROTEIN UL93	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	31-71	319-293						
HYPOTHETICAL PROTEIN UL93	HYPOTHETICAL PROTEIN UL93	HERPESVIRUS TYPE 6 (STRAIN UGANDA-1102)	21-270							
HYPOTHETICAL PROTEIN UL96	HYPOTHETICAL PROTEIN UL96	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	51-101							
HYPOTHETICAL PROTEIN UL96	HYPOTHETICAL PROTEIN UL96	HERPESVIRUS TYPE 6 (STRAIN UGANDA-1102)	51-113							
HYPOTHETICAL GENE 33 PROTEIN	HYPOTHETICAL GENE 33 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	45-100							
HYPOTHETICAL PROTEIN UL103	HYPOTHETICAL PROTEIN UL103	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-40	758-792						
VIRION PROTEIN UL104	VIRION PROTEIN UL104	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	1-58	310-364	419-492	541-575				



[illegible]



PCGENE		ALL MOTIFS	AB Viruses (no bacteriophage)									
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	
PV101K_BWTV7	50 KD PROTEIN	APPLE CHLOROTIC LEAF SPOT VIRUS	72-106								AREA1	
PV101K_BWTV7	51 KD PROTEIN	BEET WESTERN YELLOWS VIRUS (ISOLATE FL-1)	112-147		196-233						AREA2	
PV101K_BWTV7	51 KD PROTEIN	BEET WESTERN YELLOWS VIRUS (ISOLATE GB1)	112-147		196-233						AREA3	
PV101K_BWTV7	51 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN 1)	47-81		431-473						AREA4	
PV101K_BWTV7	54 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	47-81		431-473						AREA5	
PV101K_BWTV7	54 KD PROTEIN	POTATO LEAFROLL VIRUS (ISOLATE FL-1)	128-162		322-371						AREA6	
PV101K_BWTV7	54 KD PROTEIN	BABLEY STRIPE MOSAIC VIRUS	480-521								AREA7	
PV101K_BWTV7	64.1 KD PROTEIN	BEET WESTERN YELLOWS VIRUS (ISOLATE FL-1)	98-144		514-548						AREA8	
PV101K_BWTV7	64.7 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN 1)	98-144		409-443						AREA9	
PV101K_BWTV7	69.7 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	107-141									
PV101K_BWTV7	69.7 KD PROTEIN	ALFALFA MOSAIC VIRUS (STRAIN 435 / ISOLATE LEIDEN)	32-66		331-375							
PV101K_BWTV7	90 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	32-66		331-375							
PV101K_BWTV7	PROTEIN A4	VACCINIA VIRUS (STRAIN WA)	32-66		331-375							
PV101K_BWTV7	PROTEIN A4	VARIOLA VIRUS	32-66		331-375							
PV101K_BWTV7	PROTEIN A4	VACCINIA VIRUS (STRAIN COPENHAGEN)	97-213		314-355							
PV101K_BWTV7	PROTEIN A4	VACCINIA VIRUS (STRAIN WA)	96-212		313-354							
PV101K_BWTV7	PROTEIN A4	VARIOLA VIRUS	97-213		313-355							
PV101K_BWTV7	PROTEIN A4	VACCINIA VIRUS (STRAIN COPENHAGEN)	176-236									
PV101K_BWTV7	PROTEIN A4	VARIOLA VIRUS	176-236									
PV101K_BWTV7	PROTEIN A4	VACCINIA VIRUS (STRAIN COPENHAGEN)	46-91									
PV101K_BWTV7	PROTEIN A4	VARIOLA VIRUS	46-91									
PV101K_BWTV7	PROTEIN A4	VACCINIA VIRUS (STRAIN COPENHAGEN)	97-213		314-355							
PV101K_BWTV7	PROTEIN A4	VARIOLA VIRUS	96-212		313-354							
PV101K_BWTV7	PROTEIN A4	VACCINIA VIRUS (STRAIN COPENHAGEN)	114-148									
PV101K_BWTV7	PROTEIN A4	VARIOLA VIRUS	111-152									
PV101K_BWTV7	PROTEIN A4	VACCINIA VIRUS (STRAIN COPENHAGEN)	431-467									
PV101K_BWTV7	56 KD ABORTIVE LATE PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	307-341		431-467							
PV101K_BWTV7	56 KD ABORTIVE LATE PROTEIN	VARIOLA VIRUS	307-341		431-467							
PV101K_BWTV7	56 KD ABORTIVE LATE PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	1-67									
PV101K_BWTV7	PROTEIN A20	VARIOLA VIRUS	1-67									
PV101K_BWTV7	PROTEIN A20	VACCINIA VIRUS (STRAIN COPENHAGEN)	28-69									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	39-80									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	95-141		173-207		235-269					
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	95-141		173-207		235-269					
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	18-126									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	217-331									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN WA)	61-97		109-133							
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN WA)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									
PV101K_BWTV7	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-67									
PV101K_BWTV7	PROTEIN A22	VARIOLA VIRUS	26-67									



### ALLMOTIS

FCGENE	ALLIOTIS	All Virus (as Bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7
FILENAME	PROTEIN	VIRUS	62-96	143-144					AREA.1
PVA09_VACC	PROTEIN A1	VARIOLA VIRUS	1-40	124-160					
PVA09_VACC	PROTEIN A49	VACCINIA VIRUS (STRAIN COPENHAGEN)	1-40	124-160					
PVA09_VACC	PROTEIN A49	VACCINIA VIRUS (STRAIN WA)	1-40	124-160					
PVA32_VACC	PROTEIN A49	VARIOLA VIRUS	1-40	124-160					
PVA32_VACC	PROTEIN A32	VACCINIA VIRUS (STRAIN COPENHAGEN)	91-132						
PVA32_VACC	PROTEIN A32	VACCINIA VIRUS (STRAIN WA)	91-132						
PVA37_VACC	PROTEIN A32	VACCINIA VIRUS (STRAIN COPENHAGEN)	134-168						
PVA37_VACC	GUANYLATE KINASE HOMOLOG	VACCINIA VIRUS (STRAIN WA)	134-168						
PVAL1_NSVK	GUANYLATE KINASE HOMOLOG	VACCINIA VIRUS (STRAIN WA)	230-269						
PVAL1_NSVN	ALI PROTEIN	MAIZE STREAK VIRUS (KENYAN ISOLATE)	230-269						
PVAL1_NSVN	ALI PROTEIN	MAIZE STREAK VIRUS (NIGERIAN ISOLATE)	230-269						
PVAL1_NSVN	ALI PROTEIN	MAIZE STREAK VIRUS (SOUTH-AFRICAN ISOLATE)	230-269						
PVAL1_SLCV	ALI PROTEIN	SQUASH LEAF CURL VIRUS	117-131						
PVAL1_TYUVA	ALI PROTEIN	TABACCO YELLOW DWARF VIRUS (STRAIN AUSTRALIA)	191-223						
PVAL1_TYUVA	ALI PROTEIN	ABUTILON MOSAIC VIRUS (ISOLATE WEST INDIA)	44-78						
PVAL1_TYUVA	ALI PROTEIN	BEAN GOLDEN MOSAIC VIRUS	44-78						
PVAL3_PVAIV	ALI PROTEIN	POTATO YELLOW MOSAIC VIRUS (ISOLATE VENEZUELA)	10-78						
PVAL3_SLCV	ALI PROTEIN	SQUASH LEAF CURL VIRUS	44-80						
PVAL3_TGNV	ALI PROTEIN	TOMATO GOLDEN MOSAIC VIRUS	44-78						
PVAL3_TGNV	ALI PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CH-1811)	32-70						
PVAL3_TGNV	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DFR)	32-70						
PVAL3_TGNV	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN BBC)	32-70						
PVAL3_TGNV	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN NY151)	32-70						
PVAL3_TGNV	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN PV107)	32-70						
PVAL3_TGNV	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	32-70						
PVAL3_TGNV	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN W246)	32-70						
PVAL3_TGNV	APHID TRANSMISSION PROTEIN	CARNATION ETCHED RING VIRUS	99-130						
PVAL3_TGNV	APHID TRANSMISSION PROTEIN	VACCINIA VIRUS (STRAIN WA)	100-142						
PVB03_VACC	PROTEIN B3	VACCINIA VIRUS (STRAIN COPENHAGEN)	89-123						
PVB04_VACC	PROTEIN B4	VACCINIA VIRUS (STRAIN WA)	89-123						
PVB04_VACC	PROTEIN B4	VACCINIA VIRUS (STRAIN WA)	89-123						
PVB04_VACC	PROTEIN B4	VARIOLA VIRUS	89-123						
PVB05_VACC	PROTEIN B4	VACCINIA VIRUS (STRAIN LCT160)	354-398						
PVB05_VACC	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	354-398						
PVB05_VACC	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN LISTER)	354-398						
PVB05_VACC	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN WA)	354-398						
PVB07_VACC	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN WA) AND (STRAIN COPENHAGEN)	28-63						
PVB08_VACC	PROTEIN B7 PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	36-60						
PVB08_VACC	PROTEIN B8 PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	36-60						
PVB18_VACC	PROTEIN B8 PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	37-375						
PVB18_VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN WA)	37-375						
PVB18_VACC	PROTEIN B8	VARIOLA VIRUS	37-375						
PVB19_VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN COPENHAGEN)	37-375						
PVB19_VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN DAIREM 1)	37-375						
PVB19_VACC	PROTEIN B8	VACCINIA VIRUS (STRAIN WA)	37-375						
PVB30_VACC	PROTEIN B29	VACCINIA VIRUS (STRAIN COPENHAGEN)	48-83						
PVB31_VACC	PROTEIN B29	VACCINIA VIRUS (STRAIN WA)	48-83						
PVB31_VACC	PROTEIN B71	VACCINIA VIRUS (STRAIN COPENHAGEN)	61-93						
PVB31_VACC	PROTEIN B71	BEAN GOLDEN MOSAIC VIRUS	159-193						
PVB31_VACC	PROTEIN B71	SQUASH LEAF CURL VIRUS	159-193						
PVB31_VACC	PROTEIN B71	TOMATO GOLDEN MOSAIC VIRUS	159-193						
PVB31_VACC	PROTEIN B71	BEAN GOLDEN MOSAIC VIRUS	172-206						
PVB31_VACC	PROTEIN B71	SQUASH LEAF CURL VIRUS	20-41						
PVB31_VACC	PROTEIN B71	TOMATO GOLDEN MOSAIC VIRUS	35-59						
PVB31_VACC	PROTEIN B71	VACCINIA VIRUS (STRAIN COPENHAGEN)	37-42						
PVB31_VACC	PROTEIN C3	VACCINIA VIRUS (STRAIN COPENHAGEN)	263-302						
PVB31_VACC	PROTEIN C3	VACCINIA VIRUS (STRAIN COPENHAGEN)	391-412						



PCGENE	ALLNOTES	AB Virus (no description)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILE NAME	PROTEIN	VIRUS	37-42	242-292	391-442					
PC01 SFVKA	PROTEIN C2	VACCINIA VIRUS (STRAIN WR)	173-223	374-408						
PC02 VACCC	PROTEIN C4	SHOE FIBRONA VIRUS (STRAIN KASZA)	12-46							
PC03 VACCV	PROTEIN C4	VACCINIA VIRUS (STRAIN COPENHAGEN)	12-46							
PC04 VARV	PROTEIN C4	VACCINIA VIRUS (STRAIN WR)	12-46							
PC05 SFVKA	PROTEIN C4	VARIOLA VIRUS	92-123							
PC06 VACCC	PROTEIN C4	SHOE FIBRONA VIRUS (STRAIN KASZA)	31-48							
PC07 VACCV	PROTEIN C3	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-48							
PC08 VARV	PROTEIN C3	VACCINIA VIRUS (STRAIN WR)	32-70	32-121						
PC09 SFVKA	PROTEIN C3	VARIOLA VIRUS	43-86							
PC10 SFVKA	PROTEIN C1	SHOE FIBRONA VIRUS (STRAIN KASZA)	63-106							
PC11 SFVKA	HYPOTHEICAL PROTEIN C1	SHOE FIBRONA VIRUS (STRAIN KASZA)	63-106	389-215	374-412					
PC12 VACCC	HYPOTHEICAL PROTEIN C1	VACCINIA VIRUS (STRAIN COPENHAGEN)	62-116	168-226	389-215					
PC13 VACCC	PROTEIN C9	VACCINIA VIRUS (STRAIN WR)	62-116	168-226	389-215					
PC14 VACCV	PROTEIN C9	VACCINIA VIRUS (STRAIN WR)	126-180							
PC15 VACCV	PROTEIN C10	VACCINIA VIRUS (STRAIN COPENHAGEN)	126-178							
PC16 VARV	PROTEIN C10	VACCINIA VIRUS (STRAIN WR)	136-170							
PC17 SFVKA	PROTEIN C11	VARIOLA VIRUS	2-36	137-182	189-240					
PC18 SFVKA	HYPOTHEICAL PROTEIN C11	SHOE FIBRONA VIRUS (STRAIN KASZA)	2-46							
PC19 VACCC	PROTEIN C13	SHOE FIBRONA VIRUS (STRAIN COPENHAGEN)	142-178							
PC20 VACCC	PROTEIN C13	VACCINIA VIRUS (STRAIN COPENHAGEN)	100-155	375-359						
PC21 VACCV	PROTEIN C17B3	VACCINIA VIRUS (STRAIN COPENHAGEN)	40-98							
PC22 SFVKA	PROTEIN C17B3	VACCINIA VIRUS (STRAIN COPENHAGEN)	56-97							
PC23 VACCC	PROTEIN C17B3	SHOE FIBRONA VIRUS (STRAIN KASZA)	210-232							
PC24 VACCV	PROTEIN C19	VACCINIA VIRUS (STRAIN COPENHAGEN)	150-184	670-709						
PC25 SFVKA	PROTEIN C19B3	EPSTEIN-BARR VIRUS (STRAIN B95-9)	136-174	191-225	260-294					
PC26 VACCC	MAJOR CAPSID PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	116-175	308-356						
PC27 VACCV	MAJOR CAPSID PROTEIN	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	136-174	230-266	211-232					
PC28 VACCV	MAJOR CAPSID PROTEIN	HERPES SIMPLEX VIRUS	150-184	304-332						
PC29 VACCV	MAJOR CAPSID PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD-1P)	479-520	673-714	751-799					
PC30 VACCV	MAJOR CAPSID PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	105-160	293-326						
PC31 VACCV	MAJOR CAPSID PROTEIN	PSUEDOLABIES VIRUS (STRAIN DUNIAS)	128-158	316-350						
PC32 VACCV	MAJOR CAPSID PROTEIN	VARIOLA VIRUS	145-181							
PC33 VACCV	MAJOR CAPSID PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	122-157							
PC34 VACCV	MAJOR CAPSID PROTEIN	VACCINIA VIRUS (STRAIN WR)	123-157							
PC35 VACCV	MAJOR CAPSID PROTEIN	VARIOLA VIRUS	123-157							
PC36 VACCV	MAJOR CAPSID PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	126-160							
PC37 VACCV	MAJOR CAPSID PROTEIN	VACCINIA VIRUS (STRAIN WR)	126-160							
PC38 VACCV	MAJOR CAPSID PROTEIN	VARIOLA VIRUS	65-99	168-222						
PC39 VACCV	MAJOR CAPSID PROTEIN	FOWLPOX VIRUS (STRAIN FP-1)	4-32							
PC40 VACCV	MAJOR CAPSID PROTEIN	SHOE FIBRONA VIRUS (STRAIN KASZA)	67-103							
PC41 VACCV	MAJOR CAPSID PROTEIN	VARIOLA VIRUS	1-33							
PC42 VACCV	MAJOR CAPSID PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CH-1841)	1-33							
PC43 VACCV	MAJOR CAPSID PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DH)	1-33							
PC44 VACCV	MAJOR CAPSID PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN BDC)	1-33							
PC45 VACCV	MAJOR CAPSID PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN NY8151)	1-33							
PC46 VACCV	MAJOR CAPSID PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	282-316							
PC47 VACCV	MAJOR CAPSID PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	282-316							
PC48 VACCV	MAJOR CAPSID PROTEIN	VACCINIA VIRUS (STRAIN WR)	17-41							
PC49 VACCV	MAJOR CAPSID PROTEIN	VARIOLA VIRUS	17-41							
PC50 VACCV	MAJOR CAPSID PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	17-41							
PC51 VACCV	MAJOR CAPSID PROTEIN	VACCINIA VIRUS (STRAIN WR)	17-41							
PC52 VACCV	MAJOR CAPSID PROTEIN	VACCINIA VIRUS (STRAIN WR)	17-41							



[illegible]



[illegible]







AREA 1		AREA 2		AREA 3		AREA 4		AREA 5		AREA 6		AREA 7		AREA 8		AREA 9		AREA 10		AREA 11		AREA 12		AREA 13		AREA 14		AREA 15		AREA 16		AREA 17		AREA 18		AREA 19		AREA 20		AREA 21		AREA 22		AREA 23		AREA 24		AREA 25		AREA 26		AREA 27		AREA 28		AREA 29		AREA 30		AREA 31		AREA 32		AREA 33		AREA 34		AREA 35		AREA 36		AREA 37		AREA 38		AREA 39		AREA 40		AREA 41		AREA 42		AREA 43		AREA 44		AREA 45		AREA 46		AREA 47		AREA 48		AREA 49		AREA 50		AREA 51		AREA 52		AREA 53		AREA 54		AREA 55		AREA 56		AREA 57		AREA 58		AREA 59		AREA 60		AREA 61		AREA 62		AREA 63		AREA 64		AREA 65		AREA 66		AREA 67		AREA 68		AREA 69		AREA 70		AREA 71		AREA 72		AREA 73		AREA 74		AREA 75		AREA 76		AREA 77		AREA 78		AREA 79		AREA 80		AREA 81		AREA 82		AREA 83		AREA 84		AREA 85		AREA 86		AREA 87		AREA 88		AREA 89		AREA 90		AREA 91		AREA 92		AREA 93		AREA 94		AREA 95		AREA 96		AREA 97		AREA 98		AREA 99		AREA 100		AREA 101		AREA 102		AREA 103		AREA 104		AREA 105		AREA 106		AREA 107		AREA 108		AREA 109		AREA 110		AREA 111		AREA 112		AREA 113		AREA 114		AREA 115		AREA 116		AREA 117		AREA 118		AREA 119		AREA 120		AREA 121		AREA 122		AREA 123		AREA 124		AREA 125		AREA 126		AREA 127		AREA 128		AREA 129		AREA 130		AREA 131		AREA 132		AREA 133		AREA 134		AREA 135		AREA 136		AREA 137		AREA 138		AREA 139		AREA 140		AREA 141		AREA 142		AREA 143		AREA 144		AREA 145		AREA 146		AREA 147		AREA 148		AREA 149		AREA 150		AREA 151		AREA 152		AREA 153		AREA 154		AREA 155		AREA 156		AREA 157		AREA 158		AREA 159		AREA 160		AREA 161		AREA 162		AREA 163		AREA 164		AREA 165		AREA 166		AREA 167		AREA 168		AREA 169		AREA 170		AREA 171		AREA 172		AREA 173		AREA 174		AREA 175		AREA 176		AREA 177		AREA 178		AREA 179		AREA 180		AREA 181		AREA 182		AREA 183		AREA 184		AREA 185		AREA 186		AREA 187		AREA 188		AREA 189		AREA 190		AREA 191		AREA 192		AREA 193		AREA 194		AREA 195		AREA 196		AREA 197		AREA 198		AREA 199		AREA 200		AREA 201		AREA 202		AREA 203		AREA 204		AREA 205		AREA 206		AREA 207		AREA 208		AREA 209		AREA 210		AREA 211		AREA 212		AREA 213		AREA 214		AREA 215		AREA 216		AREA 217		AREA 218		AREA 219		AREA 220		AREA 221		AREA 222		AREA 223		AREA 224		AREA 225		AREA 226		AREA 227		AREA 228		AREA 229		AREA 230		AREA 231		AREA 232		AREA 233		AREA 234		AREA 235		AREA 236		AREA 237		AREA 238		AREA 239		AREA 240		AREA 241		AREA 242		AREA 243		AREA 244		AREA 245		AREA 246		AREA 247		AREA 248		AREA 249		AREA 250		AREA 251		AREA 252		AREA 253		AREA 254		AREA 255		AREA 256		AREA 257		AREA 258		AREA 259		AREA 260		AREA 261		AREA 262		AREA 263		AREA 264		AREA 265		AREA 266		AREA 267		AREA 268		AREA 269		AREA 270		AREA 271		AREA 272		AREA 273		AREA 274		AREA 275		AREA 276		AREA 277		AREA 278		AREA 279		AREA 280		AREA 281		AREA 282		AREA 283		AREA 284		AREA 285		AREA 286		AREA 287		AREA 288		AREA 289		AREA 290		AREA 291		AREA 292		AREA 293		AREA 294		AREA 295		AREA 296		AREA 297		AREA 298		AREA 299		AREA 300		AREA 301		AREA 302		AREA 303		AREA 304		AREA 305		AREA 306		AREA 307		AREA 308		AREA 309		AREA 310		AREA 311		AREA 312		AREA 313		AREA 314		AREA 315		AREA 316		AREA 317		AREA 318		AREA 319		AREA 320		AREA 321		AREA 322		AREA 323		AREA 324		AREA 325		AREA 326		AREA 327		AREA 328		AREA 329		AREA 330		AREA 331		AREA 332		AREA 333		AREA 334		AREA 335		AREA 336		AREA 337		AREA 338		AREA 339		AREA 340		AREA 341		AREA 342		AREA 343		AREA 344		AREA 345		AREA 346		AREA 347		AREA 348		AREA 349		AREA 350		AREA 351		AREA 352		AREA 353		AREA 354		AREA 355		AREA 356		AREA 357		AREA 358		AREA 359		AREA 360		AREA 361		AREA 362		AREA 363		AREA 364		AREA 365		AREA 366		AREA 367		AREA 368		AREA 369		AREA 370		AREA 371		AREA 372		AREA 373		AREA 374		AREA 375		AREA 376		AREA 377		AREA 378		AREA 379		AREA 380		AREA 381		AREA 382		AREA 383		AREA 384		AREA 385		AREA 386		AREA 387		AREA 388		AREA 389		AREA 390		AREA 391		AREA 392		AREA 393		AREA 394		AREA 395		AREA 396		AREA 397		AREA 398		AREA 399		AREA 400		AREA 401		AREA 402		AREA 403		AREA 404		AREA 405		AREA 406		AREA 407		AREA 408		AREA 409		AREA 410		AREA 411		AREA 412		AREA 413		AREA 414		AREA 415		AREA 416		AREA 417		AREA 418		AREA 419		AREA 420		AREA 421		AREA 422		AREA 423		AREA 424		AREA 425		AREA 426		AREA 427		AREA 428		AREA 429		AREA 430		AREA 431		AREA 432		AREA 433		AREA 434		AREA 435		AREA 436		AREA 437		AREA 438		AREA 439		AREA 440		AREA 441		AREA 442		AREA 443		AREA 444		AREA 445		AREA 446		AREA 447		AREA 448		AREA 449		AREA 450		AREA 451		AREA 452		AREA 453		AREA 454		AREA 455		AREA 456		AREA 457		AREA 458		AREA 459		AREA 460		AREA 461		AREA 462		AREA 463		AREA 464		AREA 465		AREA 466		AREA 467		AREA 468		AREA 469		AREA 470		AREA 471		AREA 472		AREA 473		AREA 474		AREA 475		AREA 476		AREA 477		AREA 478		AREA 479		AREA 480		AREA 481		AREA 482		AREA 483		AREA 484		AREA 485		AREA 486		AREA 487		AREA 488		AREA 489		AREA 490		AREA 491		AREA 492		AREA 493		AREA 494		AREA 495		AREA 496		AREA 497		AREA 498		AREA 499		AREA 500		AREA 501		AREA 502		AREA 503		AREA 504		AREA 505		AREA 506		AREA 507		AREA 508		AREA 509		AREA 510		AREA 511		AREA 512		AREA 513		AREA 514		AREA 515		AREA 516		AREA 517		AREA 518		AREA 519		AREA 520		AREA 521		AREA 522		AREA 523		AREA 524		AREA 525		AREA 526		AREA 527		AREA 528		AREA 529		AREA 530		AREA 531		AREA 532		AREA 533		AREA 534		AREA 535		AREA 536		AREA 537		AREA 538		AREA 539		AREA 540		AREA 541		AREA 542		AREA 543		AREA 544		AREA 545		AREA 546		AREA 547		AREA 548		AREA 549		AREA 550		AREA 551		AREA 552		AREA 553		AREA 554		AREA 555		AREA 556		AREA 557		AREA 558		AREA 559		AREA 560		AREA 561		AREA 562		AREA 563		AREA 564		AREA 565		AREA 566		AREA 567		AREA 568		AREA 569		AREA 570		AREA 571		AREA 572		AREA 573		AREA 574		AREA 575		AREA 576		AREA 577		AREA 578		AREA 579		AREA 580		AREA 581		AREA 582		AREA 583		AREA 584		AREA 585		AREA 586		AREA 587		AREA 588		AREA 589		AREA 590		AREA 591		AREA 592		AREA 593		AREA 594		AREA 595		AREA 596		AREA 597		AREA 598		AREA 599		AREA 600		AREA 601		AREA 602		AREA 603		AREA 604		AREA 605		AREA 606		AREA 607		AREA 608		AREA 609		AREA 610		AREA 611		AREA 612		AREA 613		AREA 614		AREA 615		AREA 616		AREA 617		AREA 618		AREA 619		AREA 620		AREA 621		AREA 622		AREA 623		AREA 624		AREA 625		AREA 626		AREA 627		AREA 628		AREA 629		AREA 630		AREA 631		AREA 632		AREA 633		AREA 634		AREA 635		AREA 636		AREA 637		AREA 638		AREA 639		AREA 640		AREA 641		AREA 642		AREA 643		AREA 644		AREA 645		AREA 646		AREA 647		AREA 648		AREA 649		AREA 650		AREA 651		AREA 652		AREA 653		AREA 654		AREA 655		AREA 656		AREA 657		AREA 658		AREA 659		AREA 660		AREA 661		AREA 662		AREA 663		AREA 664		AREA 665		AREA 666		AREA 667		AREA 668		AREA 669		AREA 670		AREA 671		AREA 672		AREA 673		AREA 674		AREA 675		AREA 676		AREA 677		AREA 678		AREA 679		AREA 680		AREA 681		AREA 682		AREA 683		AREA 684		AREA 685		AREA 686		AREA 687		AREA 688		AREA 689		AREA 690		AREA 691		AREA 692		AREA 693		AREA 694		AREA 695		AREA 696		AREA 697		AREA 698		AREA 699		AREA 700		AREA 701		AREA 702		AREA 703		AREA 704		AREA 705		AREA 706		AREA 707		AREA 708		AREA 709		AREA 710		AREA 711		AREA 712		AREA 713		AREA 714		AREA 715		AREA 716		AREA 717		AREA 718		AREA 719		AREA 720		AREA 721		AREA 722		AREA 723		AREA 724		AREA 725		AREA 726		AREA 727		AREA 728		AREA 729		AREA 730		AREA 731		AREA 732		AREA 733		AREA 734		AREA 735		AREA 736		AREA 737		AREA 738		AREA 739		AREA 740		AREA 741		AREA 742		AREA 743		AREA 744		AREA 745		AREA 746		AREA 747		AREA 748		AREA 749		AREA 750		AREA 751		AREA 752		AREA 753		AREA 754		AREA 755		AREA 756		AREA 757		AREA 758		AREA 759		AREA 760		AREA 761		AREA 762		AREA 763		AREA 764		AREA 765		AREA 766		AREA 767		AREA 768		AREA 769		AREA 770		AREA 771		AREA 772		AREA 773		AREA 774		AREA 775		AREA 776		AREA 777		AREA 778		AREA 779		AREA 780		AREA 781		AREA 782		AREA 783		AREA 784		AREA 785		AREA 786		AREA 787		AREA 788		AREA 789		AREA 790		AREA 791		AREA 792		AREA 793		AREA 794		AREA 795		AREA 796		AREA 797		AREA 798		AREA 799		AREA 800		AREA 801		AREA 802		AREA 803		AREA 804		AREA 805		AREA 806		AREA 807		AREA 808		AREA 809		AREA 810		AREA 811		AREA 812		AREA 813		AREA 814		AREA 815		AREA 816		AREA 817		AREA 818		AREA 819		AREA 820		AREA 821		AREA 822		AREA 823		AREA 824		AREA 825		AREA 826		AREA 827		AREA 828		AREA 829		AREA 830		AREA 831		AREA 832		AREA 833		AREA 834		AREA 835		AREA 836		AREA 837		AREA 838		AREA 839		AREA 840		AREA 841		AREA 842		AREA 843		AREA 844		AREA 845		AREA 846		AREA 847		AREA 848		AREA 849		AREA 850		AREA 851		AREA 852		AREA 853		AREA 854		AREA 855		AREA 856		AREA 857		AREA 858		AREA 859		AREA 860		AREA 861		AREA 862		AREA 863		AREA 864		AREA 865		AREA 866		AREA 867		AREA 868		AREA 869		AREA 870		AREA 871		AREA 872		AREA 873		AREA 874		AREA 875		AREA 876		AREA 877		AREA 878		AREA 879		AREA 880		AREA 881		AREA 882		AREA 883		AREA 884		AREA 885		AREA 886		AREA 887		AREA 888		AREA 889		AREA 890		AREA 891		AREA 892		AREA 893		AREA 894		AREA 895		AREA 896		AREA 897		AREA 898		AREA 899		AREA 900		AREA 901		AREA 902		AREA 903		AREA 904		AREA 905		AREA 906		AREA 907		AREA 908		AREA 909		AREA 910		AREA 911		AREA 912		AREA 913		AREA 914		AREA 915		AREA 916		AREA 917		AREA 918		AREA 919		AREA 920		AREA 921		AREA 922		AREA 923		AREA 924		AREA 925		AREA 926		AREA 927		AREA 928		AREA 929		AREA 930		AREA 931		AREA 932		AREA 933		AREA 934		AREA 935		AREA 936		AREA 937		AREA 938		AREA 939		AREA 940		AREA 941		AREA 942		AREA 943		AREA 944		AREA 945		AREA 946		AREA 947		AREA 948		AREA 949		AREA 950		AREA 951		AREA 952		AREA 953		AREA 954		AREA 955		AREA 956		AREA 957		AREA 958		AREA 959		AREA 960		AREA 9	
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[illegible]



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[illegible]



92



PL GENE	ALLA HOTIS	AB Virus (no bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6
PRV1	PROTEIN	VIRUS	5-16					
PRV1	PROTEIN	VACCHINIA VIRUS (STRAIN COPENHAGEN)						
PRV1	PROTEIN	REOVIRUS (TYPE 1) (STRAIN LANG)	619-643					
PRV1	PROTEIN	REOVIRUS (TYPE 2) (STRAIN DEARING)	618-638					
PRV1	PROTEIN	REOVIRUS (TYPE 3) (STRAIN DEARING)	618-643					
PRV1	PROTEIN	REOVIRUS (TYPE 4) (STRAIN DUNHES)	618-643					
PRV1	PROTEIN	REOVIRUS (TYPE 5) (STRAIN LANG)	618-643					
PRV1	PROTEIN	REOVIRUS (TYPE 6) (STRAIN DEARING)	618-643					
PRV1	PROTEIN	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A31001)	618-643					
PRV1	PROTEIN	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A3)	618-643					
PRV1	PROTEIN	TURKEY RHINOTRACHEITIS VIRUS	618-643					
PRV1	PROTEIN	CANINE DISTEMPER VIRUS (STRAIN ONDREKSTPOORT)	618-643					
PRV1	PROTEIN	INFLUENZA C VIRUS (STRAIN CUP10)	618-643					
PRV1	PROTEIN	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA VICTORIA 1/72)	618-643					
PRV1	PROTEIN	NEWCASTLE DISEASE VIRUS (STRAIN BEAUFORT 1/72)	618-643					
PRV1	PROTEIN	BOVINE PARAINFLUENZA 3 VIRUS	618-643					
PRV1	PROTEIN	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NH1 4/78)	618-643					
PRV1	PROTEIN	RABIES VIRUS (STRAIN A101)	618-643					
PRV1	PROTEIN	RABIES VIRUS (STRAIN CVS-11)	618-643					
PRV1	PROTEIN	RABIES VIRUS (STRAIN ERA)	618-643					
PRV1	PROTEIN	RABIES VIRUS (STRAIN PS)	618-643					
PRV1	PROTEIN	RABIES VIRUS (STRAIN SAD B19)	618-643					
PRV1	PROTEIN	RABIES VIRUS (STRAIN SAD B19)	618-643					
PRV1	PROTEIN	SONGJUL YELLOW FEVER VIRUS	618-643					
PRV1	PROTEIN	VEGETARIAN STONIAHITIS VIRUS (STRAIN INH 1/72)	618-643					
PRV1	PROTEIN	PORCINE CORONA VIRUS (STRAIN A101)	618-643					
PRV1	PROTEIN	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONA VIRUS	618-643					
PRV1	PROTEIN	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONA VIRUS	618-643					
PRV1	PROTEIN	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONA VIRUS	618-643					
PRV1	PROTEIN	TURKEY ENTERIC CORONA VIRUS	618-643					
PRV1	PROTEIN	HELPER INFECTION PERITONITIS VIRUS (STRAIN 79-1146)	618-643					
PRV1	PROTEIN	AVIAN INFECTION BRONCHITIS VIRUS (STRAIN 6/72)	618-643					
PRV1	PROTEIN	AVIAN INFECTION BRONCHITIS VIRUS (STRAIN BEAUFORT 1/72)	618-643					
PRV1	PROTEIN	AVIAN INFECTION BRONCHITIS VIRUS (STRAIN BEAUFORT 1/72)	618-643					
PRV1	PROTEIN	AVIAN INFECTION BRONCHITIS VIRUS (STRAIN BEAUFORT 1/72)	618-643					
PRV1	PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-1)	618-643					
PRV1	PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CN-1041)	618-643					
PRV1	PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM)	618-643					
PRV1	PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN BDC)	618-643					
PRV1	PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN NY101)	618-643					
PRV1	PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	618-643					
PRV1	PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN W790)	618-643					
PRV1	PROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DKS)	618-643					
PRV1	PROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DKS)	618-643					
PRV1	PROTEIN	SOYBEAN CHLOROTIC NOTTLE VIRUS	618-643					
PRV1	PROTEIN	DUCK HEPATITIS B VIRUS (BROWN SHANGHAI DUCK ISOLATE 5)	618-643					
PRV1	PROTEIN	DUCK HEPATITIS B VIRUS (BROWN SHANGHAI DUCK ISOLATE 5)	618-643					
PRV1	PROTEIN	DUCK HEPATITIS B VIRUS (BROWN SHANGHAI DUCK ISOLATE 5)	618-643					
PRV1	PROTEIN	DUCK HEPATITIS B VIRUS (BROWN SHANGHAI DUCK ISOLATE 5)	618-643					
PRV1	PROTEIN	GROUND SQUIRREL HEPATITIS VIRUS	618-643					
PRV1	PROTEIN	HERON HEPATITIS B VIRUS	618-643					
PRV1	PROTEIN	WOODCHUCK HEPATITIS VIRUS 1	618-643					
PRV1	PROTEIN	WOODCHUCK HEPATITIS VIRUS 1	618-643					
PRV1	PROTEIN	WOODCHUCK HEPATITIS VIRUS 1	618-643					



94



[illegible]



96



[illegible]



98







100



[illegible]



102



[illegible]



104



GENE	PROTEIN	ALL MOOTS	ALL Viruses (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA7	AREA8
GLUCANASE	HYPOHECTICAL BASHI-OR1 PROTEIN	HYPOHECTICAL BASHI-OR1 PROTEIN	FOWLPOX VIRUS ISOLATE IP-41(HUNNICHI)	99-10					
GLUCANASE	HYPOHECTICAL BASHI-OR2 PROTEIN	HYPOHECTICAL BASHI-OR2 PROTEIN	FOWLPOX VIRUS ISOLATE IP-41(HUNNICHI)	9-11					
GLUCANASE	HYPOHECTICAL BASHI-OR3 PROTEIN	HYPOHECTICAL BASHI-OR3 PROTEIN	FOWLPOX VIRUS ISOLATE IP-41(HUNNICHI)	113-109					
GLUCANASE	HYPOHECTICAL BASHI-OR4 PROTEIN	HYPOHECTICAL BASHI-OR4 PROTEIN	FOWLPOX VIRUS ISOLATE IP-41(HUNNICHI)	104-118					
GLUCANASE	HYPOHECTICAL BASHI-OR5 PROTEIN	HYPOHECTICAL BASHI-OR5 PROTEIN	FOWLPOX VIRUS ISOLATE IP-41(HUNNICHI)	102-211					
GLUCANASE	HYPOHECTICAL BASHI-OR6 PROTEIN	HYPOHECTICAL BASHI-OR6 PROTEIN	FOWLPOX VIRUS ISOLATE IP-41(HUNNICHI)	4-21					
GLUCANASE	HYPOHECTICAL BASHI-OR7 PROTEIN	HYPOHECTICAL BASHI-OR7 PROTEIN	FOWLPOX VIRUS ISOLATE IP-41(HUNNICHI)	117-113					
GLUCANASE	HYPOHECTICAL BASHI-OR8 PROTEIN	HYPOHECTICAL BASHI-OR8 PROTEIN	FOWLPOX VIRUS ISOLATE IP-41(HUNNICHI)	122-161					
GLUCANASE	HYPOHECTICAL BASHI-OR9 PROTEIN	HYPOHECTICAL BASHI-OR9 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-1) (HUMAN IL RPES VIRUS 4)	418-504					
GLUCANASE	HYPOHECTICAL BASHI-OR10 PROTEIN	HYPOHECTICAL BASHI-OR10 PROTEIN	HERPES VIRUS SAHNI (STRAIN 486-17)	107-188					
GLUCANASE	HYPOHECTICAL BASHI-OR11 PROTEIN	HYPOHECTICAL BASHI-OR11 PROTEIN	FOWLPOX VIRUS (STRAIN FE-1)	160-204					
GLUCANASE	HYPOHECTICAL BASHI-OR12 PROTEIN	HYPOHECTICAL BASHI-OR12 PROTEIN	MAKES'S DISEASE HERPES VIRUS (STRAIN DC-1) (INDIV)	178-211					
GLUCANASE	HYPOHECTICAL BASHI-OR13 PROTEIN	HYPOHECTICAL BASHI-OR13 PROTEIN	MAKES'S DISEASE HERPES VIRUS (STRAIN MD5) (INDIV)	178-211					
GLUCANASE	HYPOHECTICAL BASHI-OR14 PROTEIN	HYPOHECTICAL BASHI-OR14 PROTEIN	VACCINIA VIRUS (STRAIN W1)	32-78					
GLUCANASE	HYPOHECTICAL BASHI-OR15 PROTEIN	HYPOHECTICAL BASHI-OR15 PROTEIN	VACCINIA VIRUS (STRAIN W1)	181-227					
GLUCANASE	HYPOHECTICAL BASHI-OR16 PROTEIN	HYPOHECTICAL BASHI-OR16 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-1) (HUMAN IL RPES VIRUS 4)	16-38					
GLUCANASE	HYPOHECTICAL BASHI-OR17 PROTEIN	HYPOHECTICAL BASHI-OR17 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-1) (HUMAN IL RPES VIRUS 4)	64-123					
GLUCANASE	HYPOHECTICAL BASHI-OR18 PROTEIN	HYPOHECTICAL BASHI-OR18 PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-1) (HUMAN IL RPES VIRUS 4)	94-147					
GLUCANASE	HYPOHECTICAL BASHI-OR19 PROTEIN	HYPOHECTICAL BASHI-OR19 PROTEIN	CONJELINA YELLOW NOOTLE VIRUS (COYV1)	31-71					
GLUCANASE	HYPOHECTICAL BASHI-OR20 PROTEIN	HYPOHECTICAL BASHI-OR20 PROTEIN	CONJELINA YELLOW NOOTLE VIRUS (COYV1)	100-114					
GLUCANASE	HYPOHECTICAL BASHI-OR21 PROTEIN	HYPOHECTICAL BASHI-OR21 PROTEIN	LELYSTAD VIRUS (L.V)	16-34					
GLUCANASE	HYPOHECTICAL BASHI-OR22 PROTEIN	HYPOHECTICAL BASHI-OR22 PROTEIN	THEADOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)	70-127					
GLUCANASE	HYPOHECTICAL BASHI-OR23 PROTEIN	HYPOHECTICAL BASHI-OR23 PROTEIN	AVIAN ADENOVIRUS GALI (STRAIN PIELF5) (FOWL ADENOVIRUS)	21-47					
GLUCANASE	HYPOHECTICAL BASHI-OR24 PROTEIN	HYPOHECTICAL BASHI-OR24 PROTEIN	THEADOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)	6-31					
GLUCANASE	HYPOHECTICAL BASHI-OR25 PROTEIN	HYPOHECTICAL BASHI-OR25 PROTEIN	THEADOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)	78-122					
GLUCANASE	HYPOHECTICAL BASHI-OR26 PROTEIN	HYPOHECTICAL BASHI-OR26 PROTEIN	THEADOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)	1-43					
GLUCANASE	HYPOHECTICAL BASHI-OR27 PROTEIN	HYPOHECTICAL BASHI-OR27 PROTEIN	THEADOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)	1-43					
GLUCANASE	HYPOHECTICAL BASHI-OR28 PROTEIN	HYPOHECTICAL BASHI-OR28 PROTEIN	THEADOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)	6-30					
GLUCANASE	HYPOHECTICAL BASHI-OR29 PROTEIN	HYPOHECTICAL BASHI-OR29 PROTEIN	THEADOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)	6-30					
GLUCANASE	HYPOHECTICAL BASHI-OR30 PROTEIN	HYPOHECTICAL BASHI-OR30 PROTEIN	THEADOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)	31-72					
GLUCANASE	HYPOHECTICAL BASHI-OR31 PROTEIN	HYPOHECTICAL BASHI-OR31 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	31-72					
GLUCANASE	HYPOHECTICAL BASHI-OR32 PROTEIN	HYPOHECTICAL BASHI-OR32 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	104-137					
GLUCANASE	HYPOHECTICAL BASHI-OR33 PROTEIN	HYPOHECTICAL BASHI-OR33 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	104-137					
GLUCANASE	HYPOHECTICAL BASHI-OR34 PROTEIN	HYPOHECTICAL BASHI-OR34 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR35 PROTEIN	HYPOHECTICAL BASHI-OR35 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR36 PROTEIN	HYPOHECTICAL BASHI-OR36 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR37 PROTEIN	HYPOHECTICAL BASHI-OR37 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR38 PROTEIN	HYPOHECTICAL BASHI-OR38 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR39 PROTEIN	HYPOHECTICAL BASHI-OR39 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR40 PROTEIN	HYPOHECTICAL BASHI-OR40 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR41 PROTEIN	HYPOHECTICAL BASHI-OR41 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR42 PROTEIN	HYPOHECTICAL BASHI-OR42 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR43 PROTEIN	HYPOHECTICAL BASHI-OR43 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR44 PROTEIN	HYPOHECTICAL BASHI-OR44 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR45 PROTEIN	HYPOHECTICAL BASHI-OR45 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR46 PROTEIN	HYPOHECTICAL BASHI-OR46 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR47 PROTEIN	HYPOHECTICAL BASHI-OR47 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR48 PROTEIN	HYPOHECTICAL BASHI-OR48 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR49 PROTEIN	HYPOHECTICAL BASHI-OR49 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR50 PROTEIN	HYPOHECTICAL BASHI-OR50 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR51 PROTEIN	HYPOHECTICAL BASHI-OR51 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR52 PROTEIN	HYPOHECTICAL BASHI-OR52 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR53 PROTEIN	HYPOHECTICAL BASHI-OR53 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR54 PROTEIN	HYPOHECTICAL BASHI-OR54 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR55 PROTEIN	HYPOHECTICAL BASHI-OR55 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR56 PROTEIN	HYPOHECTICAL BASHI-OR56 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR57 PROTEIN	HYPOHECTICAL BASHI-OR57 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR58 PROTEIN	HYPOHECTICAL BASHI-OR58 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR59 PROTEIN	HYPOHECTICAL BASHI-OR59 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR60 PROTEIN	HYPOHECTICAL BASHI-OR60 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR61 PROTEIN	HYPOHECTICAL BASHI-OR61 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR62 PROTEIN	HYPOHECTICAL BASHI-OR62 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR63 PROTEIN	HYPOHECTICAL BASHI-OR63 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR64 PROTEIN	HYPOHECTICAL BASHI-OR64 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR65 PROTEIN	HYPOHECTICAL BASHI-OR65 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR66 PROTEIN	HYPOHECTICAL BASHI-OR66 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR67 PROTEIN	HYPOHECTICAL BASHI-OR67 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR68 PROTEIN	HYPOHECTICAL BASHI-OR68 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR69 PROTEIN	HYPOHECTICAL BASHI-OR69 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR70 PROTEIN	HYPOHECTICAL BASHI-OR70 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR71 PROTEIN	HYPOHECTICAL BASHI-OR71 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR72 PROTEIN	HYPOHECTICAL BASHI-OR72 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR73 PROTEIN	HYPOHECTICAL BASHI-OR73 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR74 PROTEIN	HYPOHECTICAL BASHI-OR74 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR75 PROTEIN	HYPOHECTICAL BASHI-OR75 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR76 PROTEIN	HYPOHECTICAL BASHI-OR76 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR77 PROTEIN	HYPOHECTICAL BASHI-OR77 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR78 PROTEIN	HYPOHECTICAL BASHI-OR78 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR79 PROTEIN	HYPOHECTICAL BASHI-OR79 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR80 PROTEIN	HYPOHECTICAL BASHI-OR80 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR81 PROTEIN	HYPOHECTICAL BASHI-OR81 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR82 PROTEIN	HYPOHECTICAL BASHI-OR82 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR83 PROTEIN	HYPOHECTICAL BASHI-OR83 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR84 PROTEIN	HYPOHECTICAL BASHI-OR84 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR85 PROTEIN	HYPOHECTICAL BASHI-OR85 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR86 PROTEIN	HYPOHECTICAL BASHI-OR86 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR87 PROTEIN	HYPOHECTICAL BASHI-OR87 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR88 PROTEIN	HYPOHECTICAL BASHI-OR88 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR89 PROTEIN	HYPOHECTICAL BASHI-OR89 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR90 PROTEIN	HYPOHECTICAL BASHI-OR90 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR91 PROTEIN	HYPOHECTICAL BASHI-OR91 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR92 PROTEIN	HYPOHECTICAL BASHI-OR92 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR93 PROTEIN	HYPOHECTICAL BASHI-OR93 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR94 PROTEIN	HYPOHECTICAL BASHI-OR94 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR95 PROTEIN	HYPOHECTICAL BASHI-OR95 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR96 PROTEIN	HYPOHECTICAL BASHI-OR96 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR97 PROTEIN	HYPOHECTICAL BASHI-OR97 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR98 PROTEIN	HYPOHECTICAL BASHI-OR98 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR99 PROTEIN	HYPOHECTICAL BASHI-OR99 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR100 PROTEIN	HYPOHECTICAL BASHI-OR100 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR101 PROTEIN	HYPOHECTICAL BASHI-OR101 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR102 PROTEIN	HYPOHECTICAL BASHI-OR102 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR103 PROTEIN	HYPOHECTICAL BASHI-OR103 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR104 PROTEIN	HYPOHECTICAL BASHI-OR104 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR105 PROTEIN	HYPOHECTICAL BASHI-OR105 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR106 PROTEIN	HYPOHECTICAL BASHI-OR106 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR107 PROTEIN	HYPOHECTICAL BASHI-OR107 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR108 PROTEIN	HYPOHECTICAL BASHI-OR108 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR109 PROTEIN	HYPOHECTICAL BASHI-OR109 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR110 PROTEIN	HYPOHECTICAL BASHI-OR110 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR111 PROTEIN	HYPOHECTICAL BASHI-OR111 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT)	197-231					
GLUCANASE	HYPOHECTICAL BASHI-OR112 PROTEIN	HYPOHECTICAL BASHI-OR112 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPP						



	ALL NOTES	All Viruses (see Bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
TREKONE		VIRUS	21-37							
CALIXANIE	PROTEIN	VACCINIA VIRUS (STRAIN COFENIAGEN)	3-9							
PYVBNH VACCC	HYPOTHETICAL T4 KD PROTEIN	VACCINIA VIRUS (STRAIN COFENIAGEN)	11-48							
PVAVCC VACCC	HYPOTHETICAL T4 KD PROTEIN	VACCINIA VIRUS (STRAIN COFENIAGEN)	29-80							
PVYVDG VACCC	HYPOTHETICAL S3 KD PROTEIN	VACCINIA VIRUS (STRAIN COFENIAGEN)	46-80							
PVYVDG VACCV	HYPOTHETICAL S3 KD PROTEIN	VACCINIA VIRUS (STRAIN WR)	7-41							
PVYBDC VACCV	HYPOTHETICAL T3 KD PROTEIN	VACCINIA VIRUS (STRAIN COFENIAGEN)	10-51							
PVYBD VACCC	HYPOTHETICAL T3 KD PROTEIN	VACCINIA VIRUS (STRAIN COFENIAGEN)	9-53							
PVYVA VACCC	HYPOTHETICAL S1 KD PROTEIN	VACCINIA VIRUS (STRAIN COFENIAGEN)								



**TABLE VI**

**107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY**

**FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS**



108



PCGUNE	(18)1116.4	PROTEIN	ALL Viruses (see Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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110



[illegible]



112



[illegible]



114



GENE	1011164	ALL Viruses (no description)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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PCG/GE	1975/17164	ALL Viruses (no Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
BILIRAPHE	PROTEIN	VIRUS							
PCPAC C03V	NUCLEOCAPSID PROTEIN	CAMPAIGN CONGO HEMORRHAGIC FEVER VIRUS (ISOLATE C4031)	221-221						AREA1
PCPAC C03V	NUCLEOCAPSID PROTEIN	CANINE DISTEMPER VIRUS (STRAIN ONDRI 85 (LIVOR1))	100-116						
PCPAC C03V	NUCLEOCAPSID PROTEIN	CHANDIPURA VIRUS (STRAIN 1635114)	40-74						
PCPAC C03V	NUCLEOCAPSID PROTEIN	CANINE ENTERIC CORONA VIRUS (STRAIN K316)	191-237						
PCPAC C03V	NUCLEOCAPSID PROTEIN	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONA VIRUS (STRAIN PURD)	191-237						
PCPAC C03V	NUCLEOCAPSID PROTEIN	PORCINE RESPIRATORY CORONA VIRUS (STRAIN 8413) 7004 / BRITISH ISOLAT	191-237						
PCPAC C03V	NUCLEOCAPSID PROTEIN	PORCINE RESPIRATORY QUONAVIRUS (STRAIN 8414)	191-237						
PCPAC C03V	NUCLEOCAPSID PROTEIN	DOUGRE VIRUS	231-265						
PCPAC C03V	NUCLEOCAPSID PROTEIN	FELINE INFECTIOUS PERITONITIS VIRUS (STRAIN 79-1146)	231-265						
PCPAC C03V	NUCLEOCAPSID PROTEIN	HANZARA VIRUS (ISOLATE K2180)	234-261						
PCPAC C03V	NUCLEOCAPSID PROTEIN	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN 18337)	6-31	112-141					
PCPAC C03V	NUCLEOCAPSID PROTEIN	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	6-31						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
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PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
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PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	147-174						
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PCPAC C03V	NUCLEOCAPSID PROTEIN	LASIA VIRUS (STRAIN 10514)	64-99						
PCPAC C0									



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GENE	INITIAL	AB Virus (as determined)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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GENE	IDENTITY	PROTEIN	Accession (no barcoding)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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122



[illegible]



124



[illegible]



126



PGENE	FILE NAME	10/11/14	ALL Viruses (see bacteriophage)	AKA1	AKA2	AKA3	AKA4	AKA5	AKA6	AKA7	AKA8	AKA9
PROTEIN	PROTEIN	10/11/14	VIRUS	48-75								AREA 9
19 KD PROTEIN	19 KD PROTEIN	10/11/14	TOBACCO RATTLE VIRUS (STRAIN TCN)	48-75								AREA 8
2A PROTEIN	2A PROTEIN	10/11/14	BRNAD BEAN MOTTLE VIRUS	301-328								
2A PROTEIN	2A PROTEIN	10/11/14	COMPEA CHLOROTIC MOTTLE VIRUS	178-203								
2A PROTEIN	2A PROTEIN	10/11/14	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	192-219								
2A PROTEIN	2A PROTEIN	10/11/14	PEANUT STUNT VIRUS (STRAIN J)	325-332	717-751							
2A PROTEIN	2A PROTEIN	10/11/14	TOMATO ASPENARY VIRUS	313-340	732-756							
10 KD MAJOR EARLY PROTEIN	10 KD MAJOR EARLY PROTEIN	10/11/14	HUMAN CYTOMEGALOVIRUS (STRAIN EISENHART)	194-211								
31 KD PROTEIN	31 KD PROTEIN	10/11/14	TOBACCO RATTLE VIRUS (STRAIN TCN)	130-160								
31 KD PROTEIN	31 KD PROTEIN	10/11/14	HUMAN ADENOVIRUS TYPE 41	13-42								
19 KD PROTEIN	19 KD PROTEIN	10/11/14	AFRICAN SWINE FEVER VIRUS (STRAIN BAZIN)	33-103								
19 KD PROTEIN	19 KD PROTEIN	10/11/14	AFRICAN SWINE FEVER VIRUS (STRAIN BAZIN)	3-10	173-199							
19 KD PROTEIN	19 KD PROTEIN	10/11/14	BROME MOSAIC VIRUS	11-38								
19 KD PROTEIN	19 KD PROTEIN	10/11/14	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	222-232								
19 KD PROTEIN	19 KD PROTEIN	10/11/14	CUCUMBER MOSAIC VIRUS (STRAIN N)	217-232								
19 KD PROTEIN	19 KD PROTEIN	10/11/14	CUCUMBER MOSAIC VIRUS (STRAIN O)	222-233								
19 KD PROTEIN	19 KD PROTEIN	10/11/14	CUCUMBER MOSAIC VIRUS (STRAIN V)	222-233								
19 KD PROTEIN	19 KD PROTEIN	10/11/14	AVIAN INFECTION BRONCHITIS VIRUS (STRAIN HEALTHE)	25-37								
19 KD PROTEIN	19 KD PROTEIN	10/11/14	AVIAN INFECTION BRONCHITIS VIRUS (STRAIN UNIV1960)	29-36								
19 KD PROTEIN	19 KD PROTEIN	10/11/14	AVIAN INFECTION BRONCHITIS VIRUS (STRAIN DEALJETTE)	6-31								
19 KD PROTEIN	19 KD PROTEIN	10/11/14	BABLY YELLOW DWAF VIRUS (ISOLATE PAV)	118-146								
31 KD PROTEIN	31 KD PROTEIN	10/11/14	BEE WESTERN YELLOW VIRUS (ISOLATE FL-1)	113-147	424-451							
31 KD PROTEIN	31 KD PROTEIN	10/11/14	BEE WESTERN YELLOW VIRUS (ISOLATE GR1)	113-147	424-451							
31 KD PROTEIN	31 KD PROTEIN	10/11/14	POTATO LEAFROLL VIRUS (STRAIN 1)	124-131	418-472							
31 KD PROTEIN	31 KD PROTEIN	10/11/14	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	124-131	418-472							
31 KD PROTEIN	31 KD PROTEIN	10/11/14	BABLY STRIPE MOSAIC VIRUS	128-133								
40 T KD PROTEIN	40 T KD PROTEIN	10/11/14	POTATO LEAFROLL VIRUS (STRAIN 1)	110-140								
40 T KD PROTEIN	40 T KD PROTEIN	10/11/14	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	110-140								
40 T KD PROTEIN	40 T KD PROTEIN	10/11/14	ALF ALFA MOSAIC VIRUS (STRAIN 435 / ISOLATE LEIDEN)	107-134								
PROTEIN A4	PROTEIN A4	10/11/14	VACCINIA VIRUS (STRAIN COPENHAGEN)	131-216	240-277	201-210	314-335					
PROTEIN A5	PROTEIN A5	10/11/14	VACCINIA VIRUS (STRAIN WR)	136-213	240-276	202-209	313-334					
PROTEIN A6	PROTEIN A6	10/11/14	VACCINIA VIRUS (STRAIN COPENHAGEN)	137-216	250-277	203-210	314-335					
PROTEIN A7	PROTEIN A7	10/11/14	VACCINIA VIRUS	176-208		/						
PROTEIN A8	PROTEIN A8	10/11/14	VACCINIA VIRUS	176-208								
PROTEIN A9	PROTEIN A9	10/11/14	VACCINIA VIRUS	60-93								
PROTEIN A11	PROTEIN A11	10/11/14	VACCINIA VIRUS (STRAIN COPENHAGEN)	219-283								
PROTEIN A11	PROTEIN A11	10/11/14	VACCINIA VIRUS	220-284								
34 KD ABORTIVE LATE PROTEIN	34 KD ABORTIVE LATE PROTEIN	10/11/14	VACCINIA VIRUS	440-467								
PROTEIN A30	PROTEIN A30	10/11/14	VACCINIA VIRUS (STRAIN COPENHAGEN)	8-67	330-337							
PROTEIN A30	PROTEIN A30	10/11/14	VACCINIA VIRUS	8-67	330-337							
PROTEIN A32	PROTEIN A32	10/11/14	VACCINIA VIRUS (STRAIN COPENHAGEN)	45-73								
PROTEIN A32	PROTEIN A32	10/11/14	VACCINIA VIRUS	54-81								
PROTEIN A33	PROTEIN A33	10/11/14	VACCINIA VIRUS (STRAIN COPENHAGEN)	93-144								
PROTEIN A33	PROTEIN A33	10/11/14	VACCINIA VIRUS	93-144								
PROTEIN A33	PROTEIN A33	10/11/14	VACCINIA VIRUS (STRAIN WR)	22-49								
PROTEIN A38	PROTEIN A38	10/11/14	VACCINIA VIRUS	22-49								
PROTEIN A38	PROTEIN A38	10/11/14	VACCINIA VIRUS (STRAIN WR)	13-35								
PROTEIN A38	PROTEIN A38	10/11/14	VACCINIA VIRUS (STRAIN COPENHAGEN)	88-113								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	93-144								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	93-144								
PROTEIN A34	PROTEIN A34	10/11/14	VACCINIA VIRUS (STRAIN COPENHAGEN)	87-114								
PROTEIN A34	PROTEIN A34	10/11/14	VACCINIA VIRUS (STRAIN WR)	87-114								
PROTEIN A34	PROTEIN A34	10/11/14	VACCINIA VIRUS	87-114								
PROTEIN A34	PROTEIN A34	10/11/14	VACCINIA VIRUS	120-135								
PROTEIN A34	PROTEIN A34	10/11/14	VACCINIA VIRUS	127-134								
PROTEIN A34	PROTEIN A34	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A34	PROTEIN A34	10/11/14	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS (STRAIN WR)	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS (STRAIN WR)	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/14	VACCINIA VIRUS	44-81								
PROTEIN A31	PROTEIN A31	10/11/										



PGCENE	1911194-6	ALL Viruses (not bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PROTEIN		VIRUS									
FILE NAME		VACCINIA VIRUS (STRAIN WR)	71-109								
PV339 VACC	PROTEIN A39	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-172								
PV340 VACC	PROTEIN A41	VACCINIA VIRUS (STRAIN WR)	143-172								
PV341 VACC	PROTEIN A43	VACCINIA VIRUS (STRAIN WR)	143-172								
PV342 VACC	PROTEIN A45	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV343 VACC	PROTEIN A47	VACCINIA VIRUS (STRAIN WR)	143-184								
PV344 VACC	PROTEIN A49	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV345 VACC	PROTEIN A51	VACCINIA VIRUS (STRAIN WR)	143-184								
PV346 VACC	PROTEIN A53	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV347 VACC	PROTEIN A55	VACCINIA VIRUS (STRAIN WR)	143-184								
PV348 VACC	PROTEIN A57	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV349 VACC	PROTEIN A59	VACCINIA VIRUS (STRAIN WR)	143-184								
PV350 VACC	PROTEIN A61	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV351 VACC	PROTEIN A63	VACCINIA VIRUS (STRAIN WR)	143-184								
PV352 VACC	PROTEIN A65	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV353 VACC	PROTEIN A67	VACCINIA VIRUS (STRAIN WR)	143-184								
PV354 VACC	PROTEIN A69	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV355 VACC	PROTEIN A71	VACCINIA VIRUS (STRAIN WR)	143-184								
PV356 VACC	PROTEIN A73	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV357 VACC	PROTEIN A75	VACCINIA VIRUS (STRAIN WR)	143-184								
PV358 VACC	PROTEIN A77	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV359 VACC	PROTEIN A79	VACCINIA VIRUS (STRAIN WR)	143-184								
PV360 VACC	PROTEIN A81	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV361 VACC	PROTEIN A83	VACCINIA VIRUS (STRAIN WR)	143-184								
PV362 VACC	PROTEIN A85	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV363 VACC	PROTEIN A87	VACCINIA VIRUS (STRAIN WR)	143-184								
PV364 VACC	PROTEIN A89	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV365 VACC	PROTEIN A91	VACCINIA VIRUS (STRAIN WR)	143-184								
PV366 VACC	PROTEIN A93	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV367 VACC	PROTEIN A95	VACCINIA VIRUS (STRAIN WR)	143-184								
PV368 VACC	PROTEIN A97	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV369 VACC	PROTEIN A99	VACCINIA VIRUS (STRAIN WR)	143-184								
PV370 VACC	PROTEIN A101	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV371 VACC	PROTEIN A103	VACCINIA VIRUS (STRAIN WR)	143-184								
PV372 VACC	PROTEIN A105	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV373 VACC	PROTEIN A107	VACCINIA VIRUS (STRAIN WR)	143-184								
PV374 VACC	PROTEIN A109	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV375 VACC	PROTEIN A111	VACCINIA VIRUS (STRAIN WR)	143-184								
PV376 VACC	PROTEIN A113	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV377 VACC	PROTEIN A115	VACCINIA VIRUS (STRAIN WR)	143-184								
PV378 VACC	PROTEIN A117	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV379 VACC	PROTEIN A119	VACCINIA VIRUS (STRAIN WR)	143-184								
PV380 VACC	PROTEIN A121	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV381 VACC	PROTEIN A123	VACCINIA VIRUS (STRAIN WR)	143-184								
PV382 VACC	PROTEIN A125	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV383 VACC	PROTEIN A127	VACCINIA VIRUS (STRAIN WR)	143-184								
PV384 VACC	PROTEIN A129	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV385 VACC	PROTEIN A131	VACCINIA VIRUS (STRAIN WR)	143-184								
PV386 VACC	PROTEIN A133	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV387 VACC	PROTEIN A135	VACCINIA VIRUS (STRAIN WR)	143-184								
PV388 VACC	PROTEIN A137	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV389 VACC	PROTEIN A139	VACCINIA VIRUS (STRAIN WR)	143-184								
PV390 VACC	PROTEIN A141	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV391 VACC	PROTEIN A143	VACCINIA VIRUS (STRAIN WR)	143-184								
PV392 VACC	PROTEIN A145	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV393 VACC	PROTEIN A147	VACCINIA VIRUS (STRAIN WR)	143-184								
PV394 VACC	PROTEIN A149	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV395 VACC	PROTEIN A151	VACCINIA VIRUS (STRAIN WR)	143-184								
PV396 VACC	PROTEIN A153	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV397 VACC	PROTEIN A155	VACCINIA VIRUS (STRAIN WR)	143-184								
PV398 VACC	PROTEIN A157	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV399 VACC	PROTEIN A159	VACCINIA VIRUS (STRAIN WR)	143-184								
PV400 VACC	PROTEIN A161	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV401 VACC	PROTEIN A163	VACCINIA VIRUS (STRAIN WR)	143-184								
PV402 VACC	PROTEIN A165	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV403 VACC	PROTEIN A167	VACCINIA VIRUS (STRAIN WR)	143-184								
PV404 VACC	PROTEIN A169	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV405 VACC	PROTEIN A171	VACCINIA VIRUS (STRAIN WR)	143-184								
PV406 VACC	PROTEIN A173	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV407 VACC	PROTEIN A175	VACCINIA VIRUS (STRAIN WR)	143-184								
PV408 VACC	PROTEIN A177	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV409 VACC	PROTEIN A179	VACCINIA VIRUS (STRAIN WR)	143-184								
PV410 VACC	PROTEIN A181	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV411 VACC	PROTEIN A183	VACCINIA VIRUS (STRAIN WR)	143-184								
PV412 VACC	PROTEIN A185	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV413 VACC	PROTEIN A187	VACCINIA VIRUS (STRAIN WR)	143-184								
PV414 VACC	PROTEIN A189	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV415 VACC	PROTEIN A191	VACCINIA VIRUS (STRAIN WR)	143-184								
PV416 VACC	PROTEIN A193	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV417 VACC	PROTEIN A195	VACCINIA VIRUS (STRAIN WR)	143-184								
PV418 VACC	PROTEIN A197	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV419 VACC	PROTEIN A199	VACCINIA VIRUS (STRAIN WR)	143-184								
PV420 VACC	PROTEIN A201	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV421 VACC	PROTEIN A203	VACCINIA VIRUS (STRAIN WR)	143-184								
PV422 VACC	PROTEIN A205	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV423 VACC	PROTEIN A207	VACCINIA VIRUS (STRAIN WR)	143-184								
PV424 VACC	PROTEIN A209	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV425 VACC	PROTEIN A211	VACCINIA VIRUS (STRAIN WR)	143-184								
PV426 VACC	PROTEIN A213	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV427 VACC	PROTEIN A215	VACCINIA VIRUS (STRAIN WR)	143-184								
PV428 VACC	PROTEIN A217	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV429 VACC	PROTEIN A219	VACCINIA VIRUS (STRAIN WR)	143-184								
PV430 VACC	PROTEIN A221	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV431 VACC	PROTEIN A223	VACCINIA VIRUS (STRAIN WR)	143-184								
PV432 VACC	PROTEIN A225	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV433 VACC	PROTEIN A227	VACCINIA VIRUS (STRAIN WR)	143-184								
PV434 VACC	PROTEIN A229	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV435 VACC	PROTEIN A231	VACCINIA VIRUS (STRAIN WR)	143-184								
PV436 VACC	PROTEIN A233	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV437 VACC	PROTEIN A235	VACCINIA VIRUS (STRAIN WR)	143-184								
PV438 VACC	PROTEIN A237	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV439 VACC	PROTEIN A239	VACCINIA VIRUS (STRAIN WR)	143-184								
PV440 VACC	PROTEIN A241	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV441 VACC	PROTEIN A243	VACCINIA VIRUS (STRAIN WR)	143-184								
PV442 VACC	PROTEIN A245	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV443 VACC	PROTEIN A247	VACCINIA VIRUS (STRAIN WR)	143-184								
PV444 VACC	PROTEIN A249	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV445 VACC	PROTEIN A251	VACCINIA VIRUS (STRAIN WR)	143-184								
PV446 VACC	PROTEIN A253	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV447 VACC	PROTEIN A255	VACCINIA VIRUS (STRAIN WR)	143-184								
PV448 VACC	PROTEIN A257	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV449 VACC	PROTEIN A259	VACCINIA VIRUS (STRAIN WR)	143-184								
PV450 VACC	PROTEIN A261	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV451 VACC	PROTEIN A263	VACCINIA VIRUS (STRAIN WR)	143-184								
PV452 VACC	PROTEIN A265	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV453 VACC	PROTEIN A267	VACCINIA VIRUS (STRAIN WR)	143-184								
PV454 VACC	PROTEIN A269	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV455 VACC	PROTEIN A271	VACCINIA VIRUS (STRAIN WR)	143-184								
PV456 VACC	PROTEIN A273	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV457 VACC	PROTEIN A275	VACCINIA VIRUS (STRAIN WR)	143-184								
PV458 VACC	PROTEIN A277	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV459 VACC	PROTEIN A279	VACCINIA VIRUS (STRAIN WR)	143-184								
PV460 VACC	PROTEIN A281	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV461 VACC	PROTEIN A283	VACCINIA VIRUS (STRAIN WR)	143-184								
PV462 VACC	PROTEIN A285	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV463 VACC	PROTEIN A287	VACCINIA VIRUS (STRAIN WR)	143-184								
PV464 VACC	PROTEIN A289	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV465 VACC	PROTEIN A291	VACCINIA VIRUS (STRAIN WR)	143-184								
PV466 VACC	PROTEIN A293	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV467 VACC	PROTEIN A295	VACCINIA VIRUS (STRAIN WR)	143-184								
PV468 VACC	PROTEIN A297	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV469 VACC	PROTEIN A299	VACCINIA VIRUS (STRAIN WR)	143-184								
PV470 VACC	PROTEIN A301	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV471 VACC	PROTEIN A303	VACCINIA VIRUS (STRAIN WR)	143-184								
PV472 VACC	PROTEIN A305	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV473 VACC	PROTEIN A307	VACCINIA VIRUS (STRAIN WR)	143-184								
PV474 VACC	PROTEIN A309	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV475 VACC	PROTEIN A311	VACCINIA VIRUS (STRAIN WR)	143-184								
PV476 VACC	PROTEIN A313	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV477 VACC	PROTEIN A315	VACCINIA VIRUS (STRAIN WR)	143-184								
PV478 VACC	PROTEIN A317	VACCINIA VIRUS (STRAIN COPENHAGEN)	143-184								
PV479 VACC	PROTEIN A319	VACCINIA VIRUS (STRAIN WR)	143-184					</			



[illegible]



GENE		AA Vectors (60 Nucleotides)		AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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PCGENE	1011781.4	ALL Viruses (not bacteriophages)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
ELK-RAB1	PROTEIN	VIRUS	146-176								
PV081 HBVB	GENE 3 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN A104)	146-176								
PV081 HBVB	GENE 1 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN KINTUCK V1)	146-176								
PV081 HBVB	PROTEIN G3	VACCINIA VIRUS (STRAIN COPENHAGEN)	48-75	131-161	225-289	335-389					
PV081 HBVB	PROTEIN G3	VACCINIA VIRUS	48-75	126-161	335-389	335-389					
PV081 HBVB	PROTEIN G3	ICTALURID HERPESVIRUS 1	71-98								
PV081 HBVB	PROTEIN F1	VACCINIA VIRUS (STRAIN COPENHAGEN)	108-338								
PV081 HBVB	PROTEIN F1	VACCINIA VIRUS (STRAIN NY)	171-301								
PV081 HBVB	PROTEIN F1	VACCINIA VIRUS	108-338								
PV081 HBVB	PROTEIN F1	VACCINIA VIRUS	11-43								
PV081 HBVB	PROTEIN F1	SPIROPLASMA VIRUS SPV1-REAZ B	172-304								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	172-304								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	172-304								
PV081 HBVB	PROTEIN F1	SPIROPLASMA VIRUS SPV1-REAZ B	260-317								
PV081 HBVB	PROTEIN F1	SPIROPLASMA VIRUS 4	287-314	383-410							
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	371-400	581-622	664-703	766-824					
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	31-58								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	233-390	497-528							
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	31-64	91-118							
PV081 HBVB	PROTEIN F1	AMSACTA MOOREI ENTOMOPHILUS	285-326								
PV081 HBVB	PROTEIN F1	SPIROPLASMA VIRUS SPV1-REAZ B	146-177	175-205	262-310						
PV081 HBVB	PROTEIN F1	SPIROPLASMA VIRUS 4	95-122								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	442-469								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	631-678	1081-1113							
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	2-29								
PV081 HBVB	PROTEIN F1	SPIROPLASMA VIRUS SPV1-REAZ B	15-49								
PV081 HBVB	PROTEIN F1	SPIROPLASMA VIRUS 4	18-52	87-148							
PV081 HBVB	PROTEIN F1	HERPESVIRUS SAIMIRI (STRAIN 11)	139-163								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	143-169	346-373	871-924	971-1087					
PV081 HBVB	PROTEIN F1	HERPESVIRUS SAIMIRI (STRAIN 11)	360-394								
PV081 HBVB	PROTEIN F1	AMSACTA MOOREI ENTOMOPHILUS	4-31								
PV081 HBVB	PROTEIN F1	SPIROPLASMA VIRUS SPV1-REAZ B	118-146								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	34-41	87-114							
PV081 HBVB	PROTEIN F1	HERPESVIRUS SAIMIRI (STRAIN 11)	47-74								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	582-609								
PV081 HBVB	PROTEIN F1	SPIROPLASMA VIRUS SPV1-REAZ B	63-92								
PV081 HBVB	PROTEIN F1	SPIROPLASMA VIRUS 4	56-83								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	550-584								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	477-504								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	1213-1334								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	163-268								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	1742-1769								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	261-388								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	447-481								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	318-422								
PV081 HBVB	PROTEIN F1	ICTALURID HERPESVIRUS 1	300-327								
PV081 HBVB	PROTEIN F1	SPIROPLASMA VIRUS 4	14-44								
PV081 HBVB	PROTEIN F1	AVIAN INFLUENZA BRONCHITIS VIRUS	1210-1260	2408-2433							
PV081 HBVB	PROTEIN F1	BOVINE CORONAVIRUS (STRAIN F1)	399-426	642-676	1022-1044	1278-1303					
PV081 HBVB	PROTEIN F1	BOVINE CORONAVIRUS (STRAIN L5)	399-426	642-676	1022-1044	1278-1303					
PV081 HBVB	PROTEIN F1	BOVINE CORONAVIRUS (STRAIN L5-13)	399-426	642-676	1022-1044	1278-1303					
PV081 HBVB	PROTEIN F1	BOVINE CORONAVIRUS (STRAIN QUEBEC)	399-426	642-676	1022-1044	1278-1303					
PV081 HBVB	PROTEIN F1	BOVINE CORONAVIRUS (STRAIN VACCINE)	399-426	642-676	1022-1044	1278-1303					
PV081 HBVB	PROTEIN F1	HUMAN CORONAVIRUS (STRAIN 229E)	776-797	809-831	1054-1112						
PV081 HBVB	PROTEIN F1	MURINE CORONAVIRUS MRV (STRAIN WILD TYPE 4)	642-684	1010-1092							
PV081 HBVB	PROTEIN F1	MURINE CORONAVIRUS MRV (STRAIN A39)	36-43	591-632	978-1040						
PV081 HBVB	PROTEIN F1	MURINE CORONAVIRUS MRV (STRAIN JKCV / VARIANT CL-2)	642-684	1010-1092							
PV081 HBVB	PROTEIN F1	MURINE CORONAVIRUS MRV (STRAIN JRG)	502-543	1819-251							



GENE	10/11/14	AB Virus (no bacteriophage tag)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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FIGURE	1971712d	ALL Viruses (see description)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PVGLF NDVU	FUSION GLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN ULSTER67)	511-178	406-312	307-336						
PVGLF PHOV	FUSION GLYCOPROTEIN PRECURSOR	PHOCINE DISTEMPER VIRUS	36-63	271-262							
PVGLF PHIC	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C19)	147-174	210-266							
PVGLF PHH	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 2 VIRUS	90-117	141-175	218-266	483-528					
PVGLF PHIT	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN GREEN)	90-117	141-175	218-266	483-528					
PVGLF PHIT	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN TOSHIBA)	90-117	141-175	218-266	483-528					
PVGLF PHB	FUSION GLYCOPROTEIN PRECURSOR	BOVINE PARAINFLUENZA 3 VIRUS	115-182	207-241	459-497						
PVGLF PHM	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NII 47815)	115-182	207-241	459-497						
PVGLF PHOK	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN KABETE O)	226-263	414-485							
PVGLF PHOL	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN L)	226-263	414-485							
PVGLF PHOS	FUSION GLYCOPROTEIN PRECURSOR	SENDAI VIRUS (STRAIN 2 / HOST MUTANTS)	122-149	211-245	400-507						
PVGLF PHOF	FUSION GLYCOPROTEIN PRECURSOR	SENDAI VIRUS (STRAIN FUSION4)	122-149	211-245	400-507						
PVGLF PHOH	FUSION GLYCOPROTEIN PRECURSOR	SENDAI VIRUS (STRAIN HARRIS)	122-149	211-245	400-507						
PVGLF PHOI	FUSION GLYCOPROTEIN PRECURSOR	SENDAI VIRUS (STRAIN H7)	122-149	211-245	400-507						
PVGLF PHOJ	FUSION GLYCOPROTEIN PRECURSOR	SENDAI VIRUS (STRAIN 2)	122-149	211-245	400-507						
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	SENDAI VIRUS 41	144-185	241-269	459-496						
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	SENDAI VIRUS 3 (STRAIN W)	137-171	417-444							
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	TURKEY RHINOTRACHEITIS VIRUS	124-161	193-200	457-484						
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	BOVINE EPHEMERAL FEVER VIRUS	533-537								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPENHAGEN)	92-123								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN 10337)	63-93								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RS01837)	66-107								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RS0190)	243-273								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN B40)	66-93								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 4	371-398								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	303-410								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN STREET)	489-519								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	VEICULAR STOMATITIS VIRUS (SEKOTYPE INDIANA / STRAIN GLASGOW)	472-499								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	EPSTEIN-BARR VIRUS (STRAIN B95-1)	549-578	619-648							
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	107-136	270-297							
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN TOWNE)	106-133								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	HEPES VIRUS (STRAIN 7 / STRAIN G5)	62-89	360-401							
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	HEPES VIRUS SAHARI (STRAIN 11)	388-415								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	47-111								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	BUNYA VIRUS CERNISTON	512-546	914-941	1128-1233						
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	BUNYA VIRUS LA CROSSE (ISOLATE L74)	913-946								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	BUNYA VIRUS	340-374	504-535	682-709						
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	BUNYA VIRUS	943-972								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN B-1)	72-100	893-920							
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN HDO)	72-100								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN LEE)	72-102								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	HANTAN VIRUS (STRAIN 76-118)	72-102								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	PAPAIANS NECROTIC SPOT VIRUS	628-655	1069-1101							
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	PROSPECT HILL VIRUS	66-96								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	PUNJAB VIRUS (STRAIN HALLINAS B1)	72-110								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	PUNJAB VIRUS (STRAIN SOTKAHO)	72-110								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	SEOL VIRUS (STRAIN B6-19)	511-540	691-720							
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	SEOL VIRUS (STRAIN R32)	72-100	511-540	694-721						
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	SEOL VIRUS (STRAIN SK-11)	72-100	511-540	694-721						
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	BOVINE EPHEMERAL FEVER VIRUS	531-564								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	BEANE VIRUS	48-82	1145-1179	1184-1211	1505-1532					
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	BUNIA VIRUS	14-41								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	LAKE VIRUS (STRAIN GA391)	86-113								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	LAKE VIRUS	86-113								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	LAKE VIRUS	374-375								
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	LAKE VIRUS	109-126	311-350							
PVGLF PHV	FUSION GLYCOPROTEIN PRECURSOR	LAKE VIRUS	303-338								



[illegible]



TCGENE	197111184	All Viruses (no bacteriophages)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10	AREA.11	AREA.12	AREA.13	AREA.14	AREA.15	AREA.16	AREA.17	AREA.18	AREA.19	AREA.20	AREA.21	AREA.22	AREA.23	AREA.24	AREA.25	AREA.26	AREA.27	AREA.28	AREA.29	AREA.30	AREA.31	AREA.32	AREA.33	AREA.34	AREA.35	AREA.36	AREA.37	AREA.38	AREA.39	AREA.40	AREA.41	AREA.42	AREA.43	AREA.44	AREA.45	AREA.46	AREA.47	AREA.48	AREA.49	AREA.50	AREA.51	AREA.52	AREA.53	AREA.54	AREA.55	AREA.56	AREA.57	AREA.58	AREA.59	AREA.60	AREA.61	AREA.62	AREA.63	AREA.64	AREA.65	AREA.66	AREA.67	AREA.68	AREA.69	AREA.70	AREA.71	AREA.72	AREA.73	AREA.74	AREA.75	AREA.76	AREA.77	AREA.78	AREA.79	AREA.80	AREA.81	AREA.82	AREA.83	AREA.84	AREA.85	AREA.86	AREA.87	AREA.88	AREA.89	AREA.90	AREA.91	AREA.92	AREA.93	AREA.94	AREA.95	AREA.96	AREA.97	AREA.98	AREA.99	AREA.100	AREA.101	AREA.102	AREA.103	AREA.104	AREA.105	AREA.106	AREA.107	AREA.108	AREA.109	AREA.110	AREA.111	AREA.112	AREA.113	AREA.114	AREA.115	AREA.116	AREA.117	AREA.118	AREA.119	AREA.120	AREA.121	AREA.122	AREA.123	AREA.124	AREA.125	AREA.126	AREA.127	AREA.128	AREA.129	AREA.130	AREA.131	AREA.132	AREA.133	AREA.134	AREA.135	AREA.136	AREA.137	AREA.138	AREA.139	AREA.140	AREA.141	AREA.142	AREA.143	AREA.144	AREA.145	AREA.146	AREA.147	AREA.148	AREA.149	AREA.150	AREA.151	AREA.152	AREA.153	AREA.154	AREA.155	AREA.156	AREA.157	AREA.158	AREA.159	AREA.160	AREA.161	AREA.162	AREA.163	AREA.164	AREA.165	AREA.166	AREA.167	AREA.168	AREA.169	AREA.170	AREA.171	AREA.172	AREA.173	AREA.174	AREA.175	AREA.176	AREA.177	AREA.178	AREA.179	AREA.180	AREA.181	AREA.182	AREA.183	AREA.184	AREA.185	AREA.186	AREA.187	AREA.188	AREA.189	AREA.190	AREA.191	AREA.192	AREA.193	AREA.194	AREA.195	AREA.196	AREA.197	AREA.198	AREA.199	AREA.200	AREA.201	AREA.202	AREA.203	AREA.204	AREA.205	AREA.206	AREA.207	AREA.208	AREA.209	AREA.210	AREA.211	AREA.212	AREA.213	AREA.214	AREA.215	AREA.216	AREA.217	AREA.218	AREA.219	AREA.220	AREA.221	AREA.222	AREA.223	AREA.224	AREA.225	AREA.226	AREA.227	AREA.228	AREA.229	AREA.230	AREA.231	AREA.232	AREA.233	AREA.234	AREA.235	AREA.236	AREA.237	AREA.238	AREA.239	AREA.240	AREA.241	AREA.242	AREA.243	AREA.244	AREA.245	AREA.246	AREA.247	AREA.248	AREA.249	AREA.250	AREA.251	AREA.252	AREA.253	AREA.254	AREA.255	AREA.256	AREA.257	AREA.258	AREA.259	AREA.260	AREA.261	AREA.262	AREA.263	AREA.264	AREA.265	AREA.266	AREA.267	AREA.268	AREA.269	AREA.270	AREA.271	AREA.272	AREA.273	AREA.274	AREA.275	AREA.276	AREA.277	AREA.278	AREA.279	AREA.280	AREA.281	AREA.282	AREA.283	AREA.284	AREA.285	AREA.286	AREA.287	AREA.288	AREA.289	AREA.290	AREA.291	AREA.292	AREA.293	AREA.294	AREA.295	AREA.296	AREA.297	AREA.298	AREA.299	AREA.300	AREA.301	AREA.302	AREA.303	AREA.304	AREA.305	AREA.306	AREA.307	AREA.308	AREA.309	AREA.310	AREA.311	AREA.312	AREA.313	AREA.314	AREA.315	AREA.316	AREA.317	AREA.318	AREA.319	AREA.320	AREA.321	AREA.322	AREA.323	AREA.324	AREA.325	AREA.326	AREA.327	AREA.328	AREA.329	AREA.330	AREA.331	AREA.332	AREA.333	AREA.334	AREA.335	AREA.336	AREA.337	AREA.338	AREA.339	AREA.340	AREA.341	AREA.342	AREA.343	AREA.344	AREA.345	AREA.346	AREA.347	AREA.348	AREA.349	AREA.350	AREA.351	AREA.352	AREA.353	AREA.354	AREA.355	AREA.356	AREA.357	AREA.358	AREA.359	AREA.360	AREA.361	AREA.362	AREA.363	AREA.364	AREA.365	AREA.366	AREA.367	AREA.368	AREA.369	AREA.370	AREA.371	AREA.372	AREA.373	AREA.374	AREA.375	AREA.376	AREA.377	AREA.378	AREA.379	AREA.380	AREA.381	AREA.382	AREA.383	AREA.384	AREA.385	AREA.386	AREA.387	AREA.388	AREA.389	AREA.390	AREA.391	AREA.392	AREA.393	AREA.394	AREA.395	AREA.396	AREA.397	AREA.398	AREA.399	AREA.400	AREA.401	AREA.402	AREA.403	AREA.404	AREA.405	AREA.406	AREA.407	AREA.408	AREA.409	AREA.410	AREA.411	AREA.412	AREA.413	AREA.414	AREA.415	AREA.416	AREA.417	AREA.418	AREA.419	AREA.420	AREA.421	AREA.422	AREA.423	AREA.424	AREA.425	AREA.426	AREA.427	AREA.428	AREA.429	AREA.430	AREA.431	AREA.432	AREA.433	AREA.434	AREA.435	AREA.436	AREA.437	AREA.438	AREA.439	AREA.440	AREA.441	AREA.442	AREA.443	AREA.444	AREA.445	AREA.446	AREA.447	AREA.448	AREA.449	AREA.450	AREA.451	AREA.452	AREA.453	AREA.454	AREA.455	AREA.456	AREA.457	AREA.458	AREA.459	AREA.460	AREA.461	AREA.462	AREA.463	AREA.464	AREA.465	AREA.466	AREA.467	AREA.468	AREA.469	AREA.470	AREA.471	AREA.472	AREA.473	AREA.474	AREA.475	AREA.476	AREA.477	AREA.478	AREA.479	AREA.480	AREA.481	AREA.482	AREA.483	AREA.484	AREA.485	AREA.486	AREA.487	AREA.488	AREA.489	AREA.490	AREA.491	AREA.492	AREA.493	AREA.494	AREA.495	AREA.496	AREA.497	AREA.498	AREA.499	AREA.500	AREA.501	AREA.502	AREA.503	AREA.504	AREA.505	AREA.506	AREA.507	AREA.508	AREA.509	AREA.510	AREA.511	AREA.512	AREA.513	AREA.514	AREA.515	AREA.516	AREA.517	AREA.518	AREA.519	AREA.520	AREA.521	AREA.522	AREA.523	AREA.524	AREA.525	AREA.526	AREA.527	AREA.528	AREA.529	AREA.530	AREA.531	AREA.532	AREA.533	AREA.534	AREA.535	AREA.536	AREA.537	AREA.538	AREA.539	AREA.540	AREA.541	AREA.542	AREA.543	AREA.544	AREA.545	AREA.546	AREA.547	AREA.548	AREA.549	AREA.550	AREA.551	AREA.552	AREA.553	AREA.554	AREA.555	AREA.556	AREA.557	AREA.558	AREA.559	AREA.560	AREA.561	AREA.562	AREA.563	AREA.564	AREA.565	AREA.566	AREA.567	AREA.568	AREA.569	AREA.570	AREA.571	AREA.572	AREA.573	AREA.574	AREA.575	AREA.576	AREA.577	AREA.578	AREA.579	AREA.580	AREA.581	AREA.582	AREA.583	AREA.584	AREA.585	AREA.586	AREA.587	AREA.588	AREA.589	AREA.590	AREA.591	AREA.592	AREA.593	AREA.594	AREA.595	AREA.596	AREA.597	AREA.598	AREA.599	AREA.600	AREA.601	AREA.602	AREA.603	AREA.604	AREA.605	AREA.606	AREA.607	AREA.608	AREA.609	AREA.610	AREA.611	AREA.612	AREA.613	AREA.614	AREA.615	AREA.616	AREA.617	AREA.618	AREA.619	AREA.620	AREA.621	AREA.622	AREA.623	AREA.624	AREA.625	AREA.626	AREA.627	AREA.628	AREA.629	AREA.630	AREA.631	AREA.632	AREA.633	AREA.634	AREA.635	AREA.636	AREA.637	AREA.638	AREA.639	AREA.640	AREA.641	AREA.642	AREA.643	AREA.644	AREA.645	AREA.646	AREA.647	AREA.648	AREA.649	AREA.650	AREA.651	AREA.652	AREA.653	AREA.654	AREA.655	AREA.656	AREA.657	AREA.658	AREA.659	AREA.660	AREA.661	AREA.662	AREA.663	AREA.664	AREA.665	AREA.666	AREA.667	AREA.668	AREA.669	AREA.670	AREA.671	AREA.672	AREA.673	AREA.674	AREA.675	AREA.676	AREA.677	AREA.678	AREA.679	AREA.680	AREA.681	AREA.682	AREA.683	AREA.684	AREA.685	AREA.686	AREA.687	AREA.688	AREA.689	AREA.690	AREA.691	AREA.692	AREA.693	AREA.694	AREA.695	AREA.696	AREA.697	AREA.698	AREA.699	AREA.700	AREA.701	AREA.702	AREA.703	AREA.704	AREA.705	AREA.706	AREA.707	AREA.708	AREA.709	AREA.710	AREA.711	AREA.712	AREA.713	AREA.714	AREA.715	AREA.716	AREA.717	AREA.718	AREA.719	AREA.720	AREA.721	AREA.722	AREA.723	AREA.724	AREA.725	AREA.726	AREA.727	AREA.728	AREA.729	AREA.730	AREA.731	AREA.732	AREA.733	AREA.734	AREA.735	AREA.736	AREA.737	AREA.738	AREA.739	AREA.740	AREA.741	AREA.742	AREA.743	AREA.744	AREA.745	AREA.746	AREA.747	AREA.748	AREA.749	AREA.750	AREA.751	AREA.752	AREA.753	AREA.754	AREA.755	AREA.756	AREA.757	AREA.758	AREA.759	AREA.760	AREA.761	AREA.762	AREA.763	AREA.764	AREA.765	AREA.766	AREA.767	AREA.768	AREA.769	AREA.770	AREA.771	AREA.772	AREA.773	AREA.774	AREA.775	AREA.776	AREA.777	AREA.778	AREA.779	AREA.780	AREA.781	AREA.782	AREA.783	AREA.784	AREA.785	AREA.786	AREA.787	AREA.788	AREA.789	AREA.790	AREA.791	AREA.792	AREA.793	AREA.794	AREA.795	AREA.796	AREA.797	AREA.798	AREA.799	AREA.800	AREA.801	AREA.802	AREA.803	AREA.804	AREA.805	AREA.806	AREA.807	AREA.808	AREA.809	AREA.810	AREA.811	AREA.812	AREA.813	AREA.814	AREA.815	AREA.816	AREA.817	AREA.818	AREA.819	AREA.820	AREA.821	AREA.822	AREA.823	AREA.824	AREA.825	AREA.826	AREA.827	AREA.828	AREA.829	AREA.830	AREA.831	AREA.832	AREA.833	AREA.834	AREA.835	AREA.836	AREA.837	AREA.838	AREA.839	AREA.840	AREA.841	AREA.842	AREA.843	AREA.844	AREA.845	AREA.846	AREA.847	AREA.848	AREA.849	AREA.850	AREA.851	AREA.852	AREA.853	AREA.854	AREA.855	AREA.856	AREA.857	AREA.858	AREA.859	AREA.860	AREA.861	AREA.862	AREA.863	AREA.864	AREA.865	AREA.866	AREA.867	AREA.868	AREA.869	AREA.870	AREA.871	AREA.872	AREA.873	AREA.874	AREA.875	AREA.876	AREA.877	AREA.878	AREA.879	AREA.880	AREA.881	AREA.882	AREA.883	AREA.884	AREA.885	AREA.886	AREA.887	AREA.888	AREA.889	AREA.890	AREA.891	AREA.892	AREA.893	AREA.894	AREA.895	AREA.896	AREA.897	AREA.898	AREA.899	AREA.900	AREA.901	AREA.902	AREA.903	AREA.904	AREA.905	AREA.906	AREA.907	AREA.908	AREA.909	AREA.910	AREA.911	AREA.912	AREA.913	AREA.914	AREA.915	AREA.916	AREA.917	AREA.918	AREA.919	AREA.920	AREA.921	AREA.922	AREA.923	AREA.924	AREA.925	AREA.926	AREA.927	AREA.928	AREA.929	AREA.930	AREA.931	AREA.932	AREA.933	AREA.934	AREA.935	AREA.936	AREA.937	AREA.938	AREA.939	AREA.940	AREA.941	AREA.942	AREA.943	AREA.944	AREA.945	AREA.946	AREA.947	AREA.948	AREA.949	AREA.950	AREA.951	AREA.952	AREA.953	AREA.954	AREA.955	AREA.956	AREA.957	AREA.958	AREA.959	AREA.960	AREA.961	AREA.962	AREA.963	AREA.964	AREA.965	AREA.966	AREA.967	AREA.968	AREA.969	AREA.970	AREA.971	AREA.972	AREA.973	AREA.974	AREA.975	AREA.976	AREA.977	AREA.978	AREA.979	AREA.980	AREA.981	AREA.982	AREA.983	AREA.984	AREA.985	AREA.986	AREA.987	AREA.988	AREA.989	AREA.990	AREA.991	AREA.992	AREA.993	AREA.994	AREA.995	AREA.996	AREA.997	AREA.998	AREA.999	AREA.1000
PROTEIN	PROTEIN	BOVINE PARAINFLUENZA 3 VIRUS																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								







PCGENE	10/11/78-6	All Viruses (see bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
PROTEIN	PROTEIN	INFLUENZA A VIRUS (STRAIN APARROTAL/STEVEN/71)	371-403																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							







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PCGENE	10711814	ALL Viruses (see bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
PROTEIN		VIRUS																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																</																																																																																																																																																																																																																																																																																																																																																																																																								



PGCLINE	FILE NAME	107:178:4	AB Virus (see bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
	PROTEIN		VIRUS								
PV311	ROTAVIRUS	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-3)	11-40	111-145						AREA 2
PV312	ROTAVIRUS	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN DS1)	11-40	111-145						
PV313	ROTAVIRUS	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 17 / STRAIN WA)	111-145							
PV314	ROTAVIRUS	MINOR OUTER CAPSID PROTEIN	RABBIT ROTAVIRUS (STRAIN ALADAMA)	111-145							
PV315	ROTAVIRUS	MINOR OUTER CAPSID PROTEIN	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	111-146							
PV316	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS	9-46							
PV317	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN MATSUJAMA)	12-41							
PV318	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN BELFAST)	9-41							
PV319	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN ENDERS)	9-46							
PV320	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN JEAN-LYNN)	9-46							
PV321	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN KILIAN)	9-46							
PV322	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN BRISTOL 1)	12-41							
PV323	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN MYAHARA VACCINE)	12-41							
PV324	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN RW)	9-41							
PV325	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN URABE VACCINE AM9)	12-41							
PV326	REOVIRUS	SIGMA 1 PROTEIN PRECURSOR	REOVIRUS (TYPE 3 / STRAIN DEARING)	26-63	127-168	222-259					
PV327	REOVIRUS	SIGMA 1 PROTEIN PRECURSOR	REOVIRUS (TYPE 3 / STRAIN D2/POHES)	4-104	130-193						
PV328	REOVIRUS	SIGMA 2 PROTEIN	REOVIRUS (TYPE 17 / STRAIN LANG)	4-33	112-160						
PV329	REOVIRUS	SIGMA 3 PROTEIN	REOVIRUS (TYPE 3 / STRAIN DEARING)	150-314							
PV330	REOVIRUS	SIGMA 1-3 PROTEIN	REOVIRUS (TYPE 3 / STRAIN D2/POHES)	189-316							
PV331	REOVIRUS	SIGMA 1-3 PROTEIN	REOVIRUS (TYPE 17 / STRAIN DEARING)	90-117							
PV332	REOVIRUS	SIGMA 1-3 PROTEIN	REOVIRUS (TYPE 17 / STRAIN LANG)	50-77							
PV333	CAPRIPOXVIRUS	PROTEIN T3A	CAPRIPOXVIRUS (STRAIN INS-1)	124-158							
PV334	PROTEIN T3		SHOPE FIBRINOLYTIC VIRUS (STRAIN KASZA)	150-337							
PV335	PROTEIN T3		EPSTEIN-BARR VIRUS (STRAIN B91-4)	324-390							
PV336	PROTEIN T3		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	41-451							
PV337	PROTEIN T3		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	176-301							
PV338	PROTEIN T3		ICTALUNDO HEPESVIRUS 1	710-737							
PV339	PROTEIN T3		VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	194-421							
PV340	PROTEIN T3		THELAPROTEUS TENAX VIRUS (STRAIN KRA1)	169-196							
PV341	PROTEIN T3		HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIDA)	169-196							
PV342	PROTEIN T3		SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	23-63							
PV343	PROTEIN T3		SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	4-61							
PV344	PROTEIN T3		SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	16-78							
PV345	PROTEIN T3		TOBACCO YELLOW DWARF VIRUS (STRAIN AUSTRALIA)	51-87							
PV346	PROTEIN T3		AUTOGRAFA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	85-112							
PV347	PROTEIN T3		SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	59-86							
PV348	PROTEIN T3		SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	5-39							
PV349	PROTEIN T3		AUTOGRAFA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	80-107							
PV350	PROTEIN T3		SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	77-111							
PV351	PROTEIN T3		SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	9-36	119-153						
PV352	PROTEIN T3		MAIZE STREAK VIRUS (NIGERIAN ISOLATE)	34-61							
PV353	PROTEIN T3		MAIZE STREAK VIRUS (SOUTH AFRICAN ISOLATE)	34-61							
PV354	PROTEIN T3		SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	76-103							
PV355	PROTEIN T3		SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	91-164							
PV356	PROTEIN T3		SOYBEAN CHLOROTIC MOTTLE VIRUS	118-148							
PV357	PROTEIN T3		SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	24-97							
PV358	PROTEIN T3		SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	337-367							
PV359	PROTEIN T3		AUTOGRAFA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	127-184							
PV360	PROTEIN T3		SOYBEAN CHLOROTIC MOTTLE VIRUS	132-149							
PV361	PROTEIN T3		SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	56-94							
PV362	PROTEIN T3		SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	11-121	546-573	659-700					
PV363	PROTEIN T3		SOYBEAN CHLOROTIC MOTTLE VIRUS	13-40							
PV364	PROTEIN T3		FOWLPOX VIRUS (ISOLATE IP-41)(MUNICH)	134-168							
PV365	PROTEIN T3		FOWLPOX VIRUS (ISOLATE IP-41)(MUNICH)	62-89	152-179	184-210					
PV366	PROTEIN T3		FOWLPOX VIRUS (ISOLATE IP-41)(MUNICH)	162-197	214-241						



[illegible]



**TABLE VII**

**107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY**

**(PREFERRED VIRAL SEQUENCES)**



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[illegible]



[illegible]



[illegible]



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ICGENE	IDENTIFIED	ALL Viruses (see Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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150



[illegible]



152



GENE	PROTEIN	121-114-4	ALL Viruses (see bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 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783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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25	ORF726	ORF727	ORF728	ORF729	ORF730	ORF731	ORF732	ORF733	ORF734	ORF735	ORF736	ORF737	ORF738	ORF739	ORF740	ORF741	ORF742	ORF743	ORF744	ORF745	ORF746	ORF747	ORF748	ORF749	ORF750	ORF751	ORF752	ORF753	ORF754	ORF755	ORF756	ORF757	ORF758	ORF759	ORF760	ORF761	ORF762	ORF763	ORF764	ORF765	ORF766	ORF767	ORF768	ORF769	ORF770	ORF771	ORF772	ORF773	ORF774	ORF775	ORF776	ORF777	ORF778	ORF779	ORF780	ORF781	ORF782	ORF783	ORF784	ORF785	ORF786	ORF787	ORF788	ORF789	ORF790	ORF791	ORF792	ORF793	ORF794	ORF795	ORF796	ORF797	ORF798	ORF799	ORF800	ORF801	ORF802	ORF803	ORF804	ORF805	ORF806	ORF807	ORF808	ORF809	ORF810	ORF811	ORF812	ORF813	ORF814	ORF815	ORF816	ORF817	ORF818	ORF819	ORF820	ORF821	ORF822	ORF823	ORF824	ORF825	ORF826	ORF827	ORF828	ORF829	ORF830	ORF831	ORF832	ORF833	ORF834	ORF835	ORF836	ORF837	ORF838	ORF839	ORF840	ORF841	ORF842	ORF843	ORF844	ORF845	ORF846	ORF847	ORF848	ORF849	ORF850	ORF851	ORF852	ORF853	ORF854	ORF855	ORF856	ORF857	ORF858	ORF859	ORF860	ORF861	ORF862	ORF863	ORF864	ORF865	ORF866	ORF867	ORF868	ORF869	ORF870	ORF871	ORF872	ORF873	ORF874	ORF875	ORF876	ORF877	ORF878	ORF879	ORF880	ORF881	ORF882	ORF883	ORF884	ORF885	ORF886	ORF887	ORF888	ORF889	ORF890	ORF891	ORF892	ORF893	ORF894	ORF895	ORF896	ORF897	ORF898	ORF899	ORF900	ORF901	ORF902	ORF903	ORF904	ORF905	ORF906	ORF907	ORF908	ORF909	ORF910	ORF911	ORF912	ORF913	ORF914	ORF915	ORF916	ORF917	ORF918	ORF919	ORF920	ORF921	ORF922	ORF923	ORF924	ORF925	ORF926	ORF927	ORF928	ORF929	ORF930	ORF931	ORF932	ORF933	ORF934	ORF935	ORF936	ORF937	ORF938	ORF939	ORF940	ORF941	ORF942	ORF943	ORF944	ORF945	ORF946	ORF947	ORF948	ORF949	ORF950	ORF951	ORF952	ORF953	ORF954	ORF955	ORF956	ORF957	ORF958	ORF959	ORF960	ORF961	ORF962	ORF963	ORF964	ORF965	ORF966	ORF967	ORF968	ORF969	ORF970	ORF971	ORF972	ORF973	ORF974	ORF975	ORF976	ORF977	ORF978	ORF979	ORF980	ORF981	ORF982	ORF983	ORF984	ORF985	ORF986	ORF987	ORF988	ORF989	ORF990	ORF991	ORF992	ORF993	ORF994	ORF995	ORF996	ORF997	ORF998	ORF999	ORF1000	ORF1001	ORF1002	ORF1003	ORF1004	ORF1005	ORF1006	ORF1007	ORF1008	ORF1009	ORF1010	ORF1011	ORF1012	ORF1013	ORF1014	ORF1015	ORF1016	ORF1017	ORF1018	ORF1019	ORF1020	ORF1021	ORF1022	ORF1023	ORF1024	ORF1025	ORF1026	ORF1027	ORF1028	ORF1029	ORF1030	ORF1031	ORF1032	ORF1033	ORF1034	ORF1035	ORF1036	ORF1037	ORF1038	ORF1039	ORF1040	ORF1041	ORF1042	ORF1043	ORF1044	ORF1045	ORF1046	ORF1047	ORF1048	ORF1049	ORF1050	ORF1051	ORF1052	ORF1053	ORF1054	ORF1055	ORF1056	ORF1057	ORF1058	ORF1059	ORF1060	ORF1061	ORF1062	ORF1063	ORF1064	ORF1065	ORF1066	ORF1067	ORF1068	ORF1069	ORF1070	ORF1071	ORF1072	ORF1073	ORF1074	ORF1075	ORF1076	ORF1077	ORF1078	ORF1079	ORF1080	ORF1081	ORF1082	ORF1083	ORF1084	ORF1085	ORF1086	ORF1087	ORF1088	ORF1089	ORF1090	ORF1091	ORF1092	ORF1093	ORF1094	ORF1095	ORF1096	ORF1097	ORF1098	ORF1099	ORF1100	ORF1101	ORF1102	ORF1103	ORF1104	ORF1105	ORF1106	ORF1107	ORF1108	ORF1109	ORF1110	ORF1111	ORF1112	ORF1113	ORF1114	ORF1115	ORF1116	ORF1117	ORF1118	ORF1119	ORF1120	ORF1121	ORF1122	ORF1123	ORF1124	ORF1125	ORF1126	ORF1127	ORF1128	ORF1129	ORF1130	ORF1131	ORF1132	ORF1133	ORF1134	ORF1135	ORF1136	ORF1137	ORF1138	ORF1139	ORF1140	ORF1141	ORF1142	ORF1143	ORF1144	ORF1145	ORF1146	ORF1147	ORF1148	ORF1149	ORF1150	ORF1151	ORF1152	ORF1153	ORF1154	ORF1155	ORF1156	ORF1157	ORF1158	ORF1159	ORF1160	ORF1161	ORF1162	ORF1163	ORF1164	ORF1165	ORF1166	ORF1167	ORF1168	ORF1169	ORF1170	ORF1171	ORF1172	ORF1173	ORF1174	ORF1175	ORF1176	ORF1177	ORF1178	ORF1179	ORF1180	ORF1181	ORF1182	ORF1183	ORF1184	ORF1185	ORF1186	ORF1187	ORF1188	ORF1189	ORF1190	ORF1191	ORF1192	ORF1193	ORF1194	ORF1195	ORF1196	ORF1197	ORF1198	ORF1199	ORF1200	ORF1201	ORF1202	ORF1203	ORF1204	ORF1205	ORF1206	ORF1207	ORF1208	ORF1209	ORF1210	ORF1211	ORF1212
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PCGENE	1971/7814	ALL Viruses (see Bacteriophage)	ABKAL	ABE1	ABE2	ABE3	ABE4	ABE5	ABE6	ABE7	ABE8	ABE9	ABE10	ABE11	ABE12	ABE13	ABE14	ABE15	ABE16	ABE17	ABE18	ABE19	ABE20	ABE21	ABE22	ABE23	ABE24	ABE25	ABE26	ABE27	ABE28	ABE29	ABE30	ABE31	ABE32	ABE33	ABE34	ABE35	ABE36	ABE37	ABE38	ABE39	ABE40	ABE41	ABE42	ABE43	ABE44	ABE45	ABE46	ABE47	ABE48	ABE49	ABE50	ABE51	ABE52	ABE53	ABE54	ABE55	ABE56	ABE57	ABE58	ABE59	ABE60	ABE61	ABE62	ABE63	ABE64	ABE65	ABE66	ABE67	ABE68	ABE69	ABE70	ABE71	ABE72	ABE73	ABE74	ABE75	ABE76	ABE77	ABE78	ABE79	ABE80	ABE81	ABE82	ABE83	ABE84	ABE85	ABE86	ABE87	ABE88	ABE89	ABE90	ABE91	ABE92	ABE93	ABE94	ABE95	ABE96	ABE97	ABE98	ABE99	ABE100	ABE101	ABE102	ABE103	ABE104	ABE105	ABE106	ABE107	ABE108	ABE109	ABE110	ABE111	ABE112	ABE113	ABE114	ABE115	ABE116	ABE117	ABE118	ABE119	ABE120	ABE121	ABE122	ABE123	ABE124	ABE125	ABE126	ABE127	ABE128	ABE129	ABE130	ABE131	ABE132	ABE133	ABE134	ABE135	ABE136	ABE137	ABE138	ABE139	ABE140	ABE141	ABE142	ABE143	ABE144	ABE145	ABE146	ABE147	ABE148	ABE149	ABE150	ABE151	ABE152	ABE153	ABE154	ABE155	ABE156	ABE157	ABE158	ABE159	ABE160	ABE161	ABE162	ABE163	ABE164	ABE165	ABE166	ABE167	ABE168	ABE169	ABE170	ABE171	ABE172	ABE173	ABE174	ABE175	ABE176	ABE177	ABE178	ABE179	ABE180	ABE181	ABE182	ABE183	ABE184	ABE185	ABE186	ABE187	ABE188	ABE189	ABE190	ABE191	ABE192	ABE193	ABE194	ABE195	ABE196	ABE197	ABE198	ABE199	ABE200	ABE201	ABE202	ABE203	ABE204	ABE205	ABE206	ABE207	ABE208	ABE209	ABE210	ABE211	ABE212	ABE213	ABE214	ABE215	ABE216	ABE217	ABE218	ABE219	ABE220	ABE221	ABE222	ABE223	ABE224	ABE225	ABE226	ABE227	ABE228	ABE229	ABE230	ABE231	ABE232	ABE233	ABE234	ABE235	ABE236	ABE237	ABE238	ABE239	ABE240	ABE241	ABE242	ABE243	ABE244	ABE245	ABE246	ABE247	ABE248	ABE249	ABE250	ABE251	ABE252	ABE253	ABE254	ABE255	ABE256	ABE257	ABE258	ABE259	ABE260	ABE261	ABE262	ABE263	ABE264	ABE265	ABE266	ABE267	ABE268	ABE269	ABE270	ABE271	ABE272	ABE273	ABE274	ABE275	ABE276	ABE277	ABE278	ABE279	ABE280	ABE281	ABE282	ABE283	ABE284	ABE285	ABE286	ABE287	ABE288	ABE289	ABE290	ABE291	ABE292	ABE293	ABE294	ABE295	ABE296	ABE297	ABE298	ABE299	ABE300	ABE301	ABE302	ABE303	ABE304	ABE305	ABE306	ABE307	ABE308	ABE309	ABE310	ABE311	ABE312	ABE313	ABE314	ABE315	ABE316	ABE317	ABE318	ABE319	ABE320	ABE321	ABE322	ABE323	ABE324	ABE325	ABE326	ABE327	ABE328	ABE329	ABE330	ABE331	ABE332	ABE333	ABE334	ABE335	ABE336	ABE337	ABE338	ABE339	ABE340	ABE341	ABE342	ABE343	ABE344	ABE345	ABE346	ABE347	ABE348	ABE349	ABE350	ABE351	ABE352	ABE353	ABE354	ABE355	ABE356	ABE357	ABE358	ABE359	ABE360	ABE361	ABE362	ABE363	ABE364	ABE365	ABE366	ABE367	ABE368	ABE369	ABE370	ABE371	ABE372	ABE373	ABE374	ABE375	ABE376	ABE377	ABE378	ABE379	ABE380	ABE381	ABE382	ABE383	ABE384	ABE385	ABE386	ABE387	ABE388	ABE389	ABE390	ABE391	ABE392	ABE393	ABE394	ABE395	ABE396	ABE397	ABE398	ABE399	ABE400	ABE401	ABE402	ABE403	ABE404	ABE405	ABE406	ABE407	ABE408	ABE409	ABE410	ABE411	ABE412	ABE413	ABE414	ABE415	ABE416	ABE417	ABE418	ABE419	ABE420	ABE421	ABE422	ABE423	ABE424	ABE425	ABE426	ABE427	ABE428	ABE429	ABE430	ABE431	ABE432	ABE433	ABE434	ABE435	ABE436	ABE437	ABE438	ABE439	ABE440	ABE441	ABE442	ABE443	ABE444	ABE445	ABE446	ABE447	ABE448	ABE449	ABE450	ABE451	ABE452	ABE453	ABE454	ABE455	ABE456	ABE457	ABE458	ABE459	ABE460	ABE461	ABE462	ABE463	ABE464	ABE465	ABE466	ABE467	ABE468	ABE469	ABE470	ABE471	ABE472	ABE473	ABE474	ABE475	ABE476	ABE477	ABE478	ABE479	ABE480	ABE481	ABE482	ABE483	ABE484	ABE485	ABE486	ABE487	ABE488	ABE489	ABE490	ABE491	ABE492	ABE493	ABE494	ABE495	ABE496	ABE497	ABE498	ABE499	ABE500	ABE501	ABE502	ABE503	ABE504	ABE505	ABE506	ABE507	ABE508	ABE509	ABE510	ABE511	ABE512	ABE513	ABE514	ABE515	ABE516	ABE517	ABE518	ABE519	ABE520	ABE521	ABE522	ABE523	ABE524	ABE525	ABE526	ABE527	ABE528	ABE529	ABE530	ABE531	ABE532	ABE533	ABE534	ABE535	ABE536	ABE537	ABE538	ABE539	ABE540	ABE541	ABE542	ABE543	ABE544	ABE545	ABE546	ABE547	ABE548	ABE549	ABE550	ABE551	ABE552	ABE553	ABE554	ABE555	ABE556	ABE557	ABE558	ABE559	ABE560	ABE561	ABE562	ABE563	ABE564	ABE565	ABE566	ABE567	ABE568	ABE569	ABE570	ABE571	ABE572	ABE573	ABE574	ABE575	ABE576	ABE577	ABE578	ABE579	ABE580	ABE581	ABE582	ABE583	ABE584	ABE585	ABE586	ABE587	ABE588	ABE589	ABE590	ABE591	ABE592	ABE593	ABE594	ABE595	ABE596	ABE597	ABE598	ABE599	ABE600	ABE601	ABE602	ABE603	ABE604	ABE605	ABE606	ABE607	ABE608	ABE609	ABE610	ABE611	ABE612	ABE613	ABE614	ABE615	ABE616	ABE617	ABE618	ABE619	ABE620	ABE621	ABE622	ABE623	ABE624	ABE625	ABE626	ABE627	ABE628	ABE629	ABE630	ABE631	ABE632	ABE633	ABE634	ABE635	ABE636	ABE637	ABE638	ABE639	ABE640	ABE641	ABE642	ABE643	ABE644	ABE645	ABE646	ABE647	ABE648	ABE649	ABE650	ABE651	ABE652	ABE653	ABE654	ABE655	ABE656	ABE657	ABE658	ABE659	ABE660	ABE661	ABE662	ABE663	ABE664	ABE665	ABE666	ABE667	ABE668	ABE669	ABE670	ABE671	ABE672	ABE673	ABE674	ABE675	ABE676	ABE677	ABE678	ABE679	ABE680	ABE681	ABE682	ABE683	ABE684	ABE685	ABE686	ABE687	ABE688	ABE689	ABE690	ABE691	ABE692	ABE693	ABE694	ABE695	ABE696	ABE697	ABE698	ABE699	ABE700	ABE701	ABE702	ABE703	ABE704	ABE705	ABE706	ABE707	ABE708	ABE709	ABE710	ABE711	ABE712	ABE713	ABE714	ABE715	ABE716	ABE717	ABE718	ABE719	ABE720	ABE721	ABE722	ABE723	ABE724	ABE725	ABE726	ABE727	ABE728	ABE729	ABE730	ABE731	ABE732	ABE733	ABE734	ABE735	ABE736	ABE737	ABE738	ABE739	ABE740	ABE741	ABE742	ABE743	ABE744	ABE745	ABE746	ABE747	ABE748	ABE749	ABE750	ABE751	ABE752	ABE753	ABE754	ABE755	ABE756	ABE757	ABE758	ABE759	ABE760	ABE761	ABE762	ABE763	ABE764	ABE765	ABE766	ABE767	ABE768	ABE769	ABE770	ABE771	ABE772	ABE773	ABE774	ABE775	ABE776	ABE777	ABE778	ABE779	ABE780	ABE781	ABE782	ABE783	ABE784	ABE785	ABE786	ABE787	ABE788	ABE789	ABE790	ABE791	ABE792	ABE793	ABE794	ABE795	ABE796	ABE797	ABE798	ABE799	ABE800	ABE801	ABE802	ABE803	ABE804	ABE805	ABE806	ABE807	ABE808	ABE809	ABE810	ABE811	ABE812	ABE813	ABE814	ABE815	ABE816	ABE817	ABE818	ABE819	ABE820	ABE821	ABE822	ABE823	ABE824	ABE825	ABE826	ABE827	ABE828	ABE829	ABE830	ABE831	ABE832	ABE833	ABE834	ABE835	ABE836	ABE837	ABE838	ABE839	ABE840	ABE841	ABE842	ABE843	ABE844	ABE845	ABE846	ABE847	ABE848	ABE849	ABE850	ABE851	ABE852	ABE853	ABE854	ABE855	ABE856	ABE857	ABE858	ABE859	ABE860	ABE861	ABE862	ABE863	ABE864	ABE865	ABE866	ABE867	ABE868	ABE869	ABE870	ABE871	ABE872	ABE873	ABE874	ABE875	ABE876	ABE877	ABE878	ABE879	ABE880	ABE881	ABE882	ABE883	ABE884	ABE885	ABE886	ABE887	ABE888	ABE889	ABE890	ABE891	ABE892	ABE893	ABE894	ABE895	ABE896	ABE897	ABE898	ABE899	ABE900	ABE901	ABE902	ABE903	ABE904	ABE905	ABE906	ABE907	ABE908	ABE909	ABE910	ABE911	ABE912	ABE913	ABE914	ABE915	ABE916	ABE917	ABE918	ABE919	ABE920	ABE921	ABE922	ABE923	ABE924	ABE925	ABE926	ABE927	ABE928	ABE929	ABE930	ABE931	ABE932	ABE933	ABE934	ABE935	ABE936	ABE937	ABE938	ABE939	ABE940	ABE941	ABE942	ABE943	ABE944	ABE945	ABE946	ABE947	ABE948	ABE949	ABE950	ABE951	ABE952	ABE953	ABE954	ABE955	ABE956	ABE957	ABE958	ABE959	ABE960	ABE961	ABE962	ABE963	ABE964	ABE965	ABE966	ABE967	ABE968	ABE969	ABE970	ABE971	ABE972	ABE973	ABE974	ABE975	ABE976	ABE977	ABE978	ABE979	ABE980	ABE981	ABE982	ABE983	ABE984	ABE985	ABE986	ABE987	ABE988	ABE989	ABE990	ABE991	ABE992	ABE993	ABE994	ABE995	ABE996	ABE997	ABE998	ABE999	ABE1000
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[illegible]



TABLE VIII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL PROCARYOTIC PROTEINS



CGENE	1971-1984	Prebarytic Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PROTEIN	120 KD SURFACE-EXPOSED PROTEIN	ORGANISM	81-110	240-298	746-118	938-632	1168-1202			
120 KD SURFACE-EXPOSED PROTEIN		RICKETTSIA RICKETTSII	61-94							
17 KD ANTIGEN PRECURSOR		RICKETTSIA TYPHI	241-268	460-487	754-781	904-931	1220-1234	1344-1371	1723-1750	
17 KD ANTIGEN PRECURSOR (CELL SURFACE)		RICKETTSIA RICKETTSII	268-298	607-634						
		DESULFOLOCCUS MOBILIS	35-52	120-147						
22.6 KD PROTEIN		VIBRIO ANGUILLARUM	151-196							
40 KD PROTEIN PRECURSOR		ESCHERICHIA COLI	511-518							
40 KD INNER-MEMBRANE PROTEIN		PROTEUS MIRABILIS	14-41							
60 KD INNER-MEMBRANE PROTEIN		ZYMOGNATHUS MOBILIS	95-122	444-224						
60 KD PROTEIN		BACILLUS SUBTILIS	24-31	218-246						
60 KD PROTEIN		ESCHERICHIA COLI	205-232							
PROB 6-PHOSPHOGLUCONATE DEHYDROGENASE		SALMONELLA TYPHIMURUM	450-477							
6-PHOSPHOGLUCONATE DEHYDROGENASE		STAPHYLOCOCCUS AUREUS	146-173	185-212						
6-PHOSPHOGLUCONATE DEHYDROGENASE		BACILLUS SP	351-378							
ASPARTATE AMINOTRANSFERASE		ESCHERICHIA COLI	176-203							
ASPARTATE AMINOTRANSFERASE		ESCHERICHIA COLI	85-126	170-204	209-233					
ABORTIVE PHAGE RESISTANCE PROTEIN ABIC		LACTOCOCCUS LACTIS	127-154							
TRANSCRIPTIONAL REPRESSION ACCR		AGROBACTERIUM TUMEFACIENS	398-432							
ISOCITRATE LYASE		ESCHERICHIA COLI	48-73							
ACONITATE HYDRATASE		BACILLUS SUBTILIS	41-48	613-640						
ACONITATE HYDRATASE		ESCHERICHIA COLI	85-112							
ACTOIN CATABOLISM REG PRO		ALCALIGENES EUTROPHUS	4-31							
ACTYL CANONER PROTEIN		ESCHERICHIA COLI	212-247							
ACQUILAVIN RESISTANCE PROTEIN A PRECURSOR		ESCHERICHIA COLI	530-551							
ACQUILAVIN RESISTANCE PROTEIN B		ESCHERICHIA COLI	512-530	726-753						
ACQUILAVIN RESISTANCE PROTEIN F		ESCHERICHIA COLI	531-544							
PUTATIVE KETOACYL REDUCTASE		STREPTOMYCES COELICOLOR	217-244	576-603						
ACTIN-ASSEMBLY INDUCING PROTEIN PRECURSOR		LISTERIA MONOCYTOGENES	119-170							
ACTIN-ASSEMBLY INDUCING PROTEIN PRECURSOR		NOCARDIA LACTAMIDURANS	198-425	434-481	527-556	1003-1032				
ACTY SYNTHETASE		BACILLUS SUBTILIS	332-344	870-901	943-977					
METHYLOXIDASE		BACILLUS SUBTILIS	174-211							
ATP-DEPENDENT NUCLEASE SUBUNIT A		BACILLUS SUBTILIS	298-325							
ATP-DEPENDENT NUCLEASE SUBUNIT B		BACILLUS SUBTILIS	631-680	778-806						
NADPH-DEPENDENT BUTANOL DEHYDROGENASE		CLOSTRIDIUM ACETOBUTYLICUM	271-298							
NADPH-DEPENDENT BUTANOL DEHYDROGENASE A		CLOSTRIDIUM ACETOBUTYLICUM	43-72	697-724	931-950	990-1017	1168-1198	1387-1414		
NADPH-DEPENDENT BUTANOL DEHYDROGENASE A		CLOSTRIDIUM ACETOBUTYLICUM	90-131							
NADPH-DEPENDENT BUTANOL DEHYDROGENASE B		CLOSTRIDIUM ACETOBUTYLICUM	1357-1384							
ALCOHOL DEHYDROGENASE		ESCHERICHIA COLI	276-307							
ALCOHOL DEHYDROGENASE		ESCHERICHIA COLI	278-305							
PUTATIVE REGULATORY PROTEIN ADIY		MYCOPLASMA PNEUMONIAE	419-433	597-633						
ADHESIN P1 PRECURSOR		MYCOPLASMA PNEUMONIAE	26-53							
ADP ATP CARRIER PROTEIN		RICKETTSIA PRAOWAZELII	139-159	163-192						
ALPHA-GALACTOSIDASE		AEROMONAS HYDROPHILA	19-46							
BETA-AGARASE PRECURSOR		STREPTOCOCCUS MUTANS	3-20	468-493	503-530					
ACCESSORY GENE REGULATORY PROTEIN		STAPHYLOCOCCUS AUREUS	51-78	908-935						
ATTACHING LOCUS PROTEIN PRECURSOR		YERSINIA ENTEROCOLITICA	5-12							
ASPARTATE AMINOTRANSFERASE		ESCHERICHIA COLI	268-316							
ASPARTATE AMINOTRANSFERASE		ESCHERICHIA COLI	160-194							
ASPARTATE AMINOTRANSFERASE		ESCHERICHIA COLI	149-176							
FRUCTOSE-BIPHOSPHATE ALDOASE		PSEUDOMONAS AERUGINOSA	81-113							
ALGINATE BIOSYNTHETIC REG PROTEIN ALGB		PSEUDOMONAS AERUGINOSA	115-142							
ALGINATE BIOSYNTHETIC REG PROTEIN ALGB		PSEUDOMONAS AERUGINOSA	131-172							
ALGINATE BIOSYNTHETIC REG PROTEIN ALGB		PSEUDOMONAS AERUGINOSA	9-36							
ALGINATE BIOSYNTHETIC REG PROTEIN ALGB		PSEUDOMONAS AERUGINOSA								
ALGINATE BIOSYNTHETIC REG PROTEIN ALGB		PSEUDOMONAS AERUGINOSA								
ALGINATE BIOSYNTHETIC REG PROTEIN ALGB		PSEUDOMONAS AERUGINOSA								
ALGINATE BIOSYNTHETIC REG PROTEIN ALGB		PSEUDOMONAS AERUGINOSA								
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ALGINATE BIOSYNTHETIC REG PROTEIN ALGB		PSEUDOMONAS AERUGINOSA								
ALGINATE BIOSYN										



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GENE	107179.4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PROKARYOTIC SEQUENCES	PROKARYOTIC SEQUENCES									
PATPD SYN1	ATP SYNTHASE DELTA CHAIN	SYNECHOCOCCUS SP	100-127							
PATPD SYN2	ATP SYNTHASE DELTA CHAIN	SYNECHOCOCCUS SP	111-147							
PATPD VIBAL	ATP SYNTHASE DELTA CHAIN	VIBRIO ALGINOLYTICUS	110-137							
PATPE BAGE1	ATP SYNTHASE EPSILON CHAIN	BACILLUS FIRMUS	51-80							
PATPE MYOGA	ATP SYNTHASE EPSILON CHAIN	MYCOPLASMA GALLISEPTICUM	99-126							
PATPE PROMO	ATP SYNTHASE EPSILON CHAIN	PROFIONIGENIUM INDESTRUCTUM	100-127							
PATPE SYN1	ATP SYNTHASE EPSILON CHAIN	SYNECHOCOCCUS SP	72-106							
PATPE ANAS1	ATP SYNTHASE B CHAIN	ANABAENA SP	11-44	137-164						
PATPE BAGE1	ATP SYNTHASE B CHAIN	BACILLUS FIRMUS	106-131							
PATPE BAGE2	ATP SYNTHASE B CHAIN	BACILLUS MEGATERIUM	35-45	172-170						
PATPE MYOGA	ATP SYNTHASE B CHAIN	MYCOPLASMA GALLISEPTICUM	82-135	170-197						
PATPE SYN1	ATP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	15-49	111-159						
PATPE SYN2	ATP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	12-39	128-155						
PATPE THEP3	ATP SYNTHASE B CHAIN PRECURSOR	THEMOPHILIC BACTERIUM PS-1	30-37							
PATPD ANAS1	ATP SYNTHASE GAMMA CHAIN	ANABAENA SP	276-310							
PATPD ECOL1	ATP SYNTHASE GAMMA CHAIN	ESCHERICHIA COLI	351-233							
PATPD MYOGA	ATP SYNTHASE GAMMA CHAIN	MYCOPLASMA GALLISEPTICUM	28-62	92-140						
PATPD RHORU	ATP SYNTHASE GAMMA CHAIN	RHODOSPIRILLUM RUBRUM	370-297							
PATPD SYN1	ATP SYNTHASE GAMMA CHAIN	SYNECHOCOCCUS SP	240-307							
PATPD MYOGA	ATP SYNTHASE GAMMA CHAIN	SYNECHOCOCCUS SP	96-126	210-307						
PATPD SYN1	ATP SYNTHASE PROTEIN I	MYCOPLASMA GALLISEPTICUM	133-167							
PATPD ANAS1	ATP SYNTHASE B' CHAIN	ANABAENA SP	128-156							
PATPD BAGE1	ATP SYNTHASE BETA CHAIN	BACILLUS FIRMUS	167-189	356-363						
PATPD RHORU	ATP SYNTHASE B' CHAIN	RHODOSPIRILLUM RUBRUM	40-74							
PATPD SYN1	ATP SYNTHASE B' CHAIN	SYNECHOCOCCUS SP	37-110	178-155						
PATPD SYN2	ATP SYNTHASE B' CHAIN	SYNECHOCOCCUS SP	70-100							
PATPD SYN3	ATP SYNTHASE B' CHAIN	SYNECHOCOCCUS SP	108-135							
PATPD BAGE1	ATP SYNTHASE PROTEIN I	BACILLUS MEGATERIUM	14-62							
PATPD SYN1	ATP SYNTHASE PROTEIN I	SYNECHOCOCCUS SP	90-131							
PATPD PLEGO	1-ALPHA-HYDROXYSTEROID DEHYDROGENASE	PEUDOMONAS SYRINGAE	184-211	237-260						
PATPD EUBSP	1-ALPHA-HYDROXYSTEROID DEHYDROGENASE	EUBACTERIUM SP	26-53							
PATPD HALLM	HALORHODOPSIN	HALOBACTERIUM HALOBILIUM	145-179							
PATPD HALLG	HALORHODOPSIN PRECURSOR	HALOBACTERIUM SP	180-214							
PATPD ECOL1	SENSOR PROTEIN BAE1	ESCHERICHIA COLI	132-186							
PATPD STRAO	IGA FC RECEPTOR PRECURSOR	STREPTOCOCCUS AGALACTIAE	92-119	138-204	267-306	343-385	487-524	562-589	1014-1041	
PATPD VITSP	BACTERIAL HEMOGLOBIN	VITREOSILLA SP	119-146							
PATPD EUBSP	BILE ACID-INDUCIBLE OPERON PROTEIN C	EUBACTERIUM SP	423-430							
PATPD ECOL1	SENSOR PROTEIN BAKA	ESCHERICHIA COLI	334-361	423-455						
PATPD ECOL1	SENSOR PROTEIN BALS	ESCHERICHIA COLI	132-156							
PATPD HALLM	PUTATIVE BACTERIO-OPERON ACTIVATOR	HALOBACTERIUM HALOBILIUM	401-442							
PATPD ECOL1	BAX PROTEIN	ESCHERICHIA COLI	21-64							
PATPD RHOC	METHYLTRANSFERASE	ESCHERICHIA COLI	6-35							
PATPD RHOC	PROTEOCHLOROPHYLLIDE REDUCTASE 46 KD CHAIN	RHODOBACTER CAPSULATUS	1000-1032							
PATPD RHOC	PROTEOCHLOROPHYLLIDE REDUCTASE 46 KD CHAIN	RHODOBACTER CAPSULATUS	240-276							
PATPD RHOC	PROTEOCHLOROPHYLL A PROTEIN	CLOSTRIDIUM PERKINGENS	71-99	585-646						
PATPD RHOC	CELLULOSE SYNTHASE OPERON C PROTEIN	PROSTHECOCHLORIS AESTUARII	61-81							
PATPD RHOC	CELLULOSE SYNTHASE OPERON D PROTEIN	ACETOBACTER XYLINUM	131-158	1035-1082						
PATPD RHOC	CELLULOSE SYNTHASE OPERON D PROTEIN	ACETOBACTER XYLINUM	10-37							
PATPD RHOC	BENZYLATE 1,3-DIOXYGENASE ALPHA SUBUNIT	ACETOBACTER CALCOACETICUS	190-217							
PATPD RHOC	HIGH AFFINITY CHOLINE TRANSPORT PROTEIN	ESCHERICHIA COLI	203-270							
PATPD RHOC	BEXA PROTEIN	HAEMOPHILUS INFLUENZAE	21-30							
PATPD RHOC	BEXC PROTEIN	HAEMOPHILUS INFLUENZAE	151-184	226-253						
PATPD RHOC	BEXD PROTEIN	HAEMOPHILUS INFLUENZAE	205-239							
PATPD RHOC	BACTERIOPEPTIDIN	HAEMOPHILUS INFLUENZAE	8-35							
PATPD RHOC	EVOLVED BETA-GALACTOSIDASE ALPHA-SUBUNIT	NITROBACTER WINOGRADESKYI	955-985							
PATPD RHOC	BETA-GALACTOSIDASE	ESCHERICHIA COLI	599-631							



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TCGENE	10761784	Prokaryotic Sequences	ABRAL	ABRAL	ABRAL	ABRAL	ABRAL	ABRAL
CHILD NAME	PROTEIN	ORGANISM	ABRAL	ABRAL	ABRAL	ABRAL	ABRAL	ABRAL
CHILD NAME	CHITINASE D PRECURSOR	BACILLUS CIRCULANS	102-161	189-216				AREA 2
CHILD NAME	CHITINASE	SACCHAROPOLYSPORA ERYTHRAEA	92-119					
CHILD NAME	CHITINASE G1 PRECURSOR	STREPTOMYCES PULICATUS	150-284					
CHILD NAME	CHITINASE MUTASE	BACILLUS SUBTILIS	7-37					
CHILD NAME	CHOLESTEROL OXIDASE PRECURSOR	BREVIDACTERIUM STEROLICUM	163-290					
CHILD NAME	CHOLEST-5-EN-3-OXIDASE	VIBRIO CHOLERAE	76-106					
CHILD NAME	CHOLEST-5-EN-3-OXIDASE	AGROBACTERIUM TUMEFACIENS	4-31	181-208				
CHILD NAME	BETA-1-4-GLUCAN EXPORT PROTEIN	AGROBACTERIUM TUMEFACIENS	100-127					
CHILD NAME	RECEPTOR PROTEIN CHIVE PRECURSOR	CITROBACTER FREUNDII	431-462					
CHILD NAME	CITROLYSIN PROTEIN 1	ESCHERICHIA COLI	146-173					
CHILD NAME	COLICIN RECEPTOR PRECURSOR	BACILLUS SUBTILIS	318-465					
CHILD NAME	PUTATIVE DNA RECOMBINASE	ACINETOBACTER ANITRATUM	143-170					
CHILD NAME	CITRATE SYNTHASE	BACILLUS COAGULANS	24-31					
CHILD NAME	CITRATE SYNTHASE	SALMONELLA TYPHIMURUM	154-181					
CHILD NAME	CITRATE-PROTON SYMPORT	KLEBSIELLA PNEUMONIAE	194-221					
CHILD NAME	CITRATE-SODIUM SYMPORT	SALMONELLA DUBLIN	194-221					
CHILD NAME	CITRATE-SODIUM SYMPORT	SALMONELLA PULLORI	194-221					
CHILD NAME	CITRATE-SODIUM SYMPORT	PSEUDOMONAS PUTIDA	13-36					
CHILD NAME	CHLOROCATECHOL 1,2-DIOXYGENASE	ESCHERICHIA COLI	133-167					
CHILD NAME	CHAIN LENGTH DETERMINANT PROTEIN	ESCHERICHIA COLI	176-212	290-237				
CHILD NAME	CHAIN LENGTH DETERMINANT PROTEIN	SALMONELLA TYPHIMURUM	96-127	131-212				
CHILD NAME	ALPHA-CLONIPAIN PRECURSOR	CLOSTRIDIUM HISTOLYTICUM	10-58	491-524				
CHILD NAME	ATP-BINDING SUBUNIT CLPA	ESCHERICHIA COLI	635-665					
CHILD NAME	CLPA RHOB	RHODOSPIRILLUM RUBRUM	419-466					
CHILD NAME	CLPA RHOB	BACTEROIDES NODULUS	116-153	442-476				
CHILD NAME	CLPB PROTEIN	ESCHERICHIA COLI	444-489	503-590				
CHILD NAME	CLPB PROTEIN	AZOTOBACTER VINELANDII	215-242	332-359				
CHILD NAME	CLPX AZOVI	ESCHERICHIA COLI	335-382					
CHILD NAME	ATP-BINDING SUBUNIT CLPX	ESCHERICHIA COLI	36-77					
CHILD NAME	P-2-CYCLO-NUC-2'-PHOSPHODIESTERASE PRECURSOR	ESCHERICHIA COLI	102-129					
CHILD NAME	COMPETENCE PROTEIN 1	BACILLUS SUBTILIS	108-125	186-213				
CHILD NAME	COMPETENCE REGULATORY PROTEIN	BACILLUS SUBTILIS	154-239					
CHILD NAME	COP A PROTEIN	STAPHYLOCOCCUS AUREUS	7-53					
CHILD NAME	COPPER RESISTANCE PROTEIN B PRECURSOR	PSEUDOMONAS SYRINGAE	140-167					
CHILD NAME	MAGNESIUM COBALT TRANSPORT PROTEIN COBA	ESCHERICHIA COLI	114-161					
CHILD NAME	MAGNESIUM COBALT TRANSPORT PROTEIN COBA	SALMONELLA TYPHIMURUM	174-181					
CHILD NAME	SPOLE COAT PROTEIN E	BACILLUS SUBTILIS	45-92					
CHILD NAME	CYTODROME C OXIDASE POLYPEPTIDE 1	BRADYRHIZOBIUM JAPONICUM	380-407					
CHILD NAME	CYTODROME C OXIDASE POLYPEPTIDE 1	PARACOCUS DENITRIFICANS	383-410					
CHILD NAME	CYTODROME C OXIDASE POLYPEPTIDE 1	RHODOBACTER SPIAEROIDES	384-423					
CHILD NAME	OXIDASE ASSEMBLY FACTOR	BACILLUS FIRMUS	36-63					
CHILD NAME	OXIDASE ASSEMBLY FACTOR	BACILLUS SUBTILIS	49-76					
CHILD NAME	CHLOROPHYLL A-SUBUNIT PROTEIN B	NEISSERIA GONORRHOEA	72-99	165-209				
CHILD NAME	MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE	ESCHERICHIA COLI	109-316					
CHILD NAME	MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE	SALMONELLA TYPHIMURUM	311-338					
CHILD NAME	SENSOR PROTEIN CPXA	ESCHERICHIA COLI	234-281					
CHILD NAME	CYTODROME P450 10C1	STREPTOMYCES SP	157-184					
CHILD NAME	4-DEOXYATRYNOLIDE B (DBE) HYDROXYLASE	BACILLUS SUBTILIS	231-260					
CHILD NAME	CYTODROME P450 10F	ANABACNA SP	240-283					
CHILD NAME	PROBABLE CYTOCHROME P450	BACILLUS THURINGIENSIS	98-125					
CHILD NAME	37 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	153-187					
CHILD NAME	19 KD INSECTICIDAL TOXIN	BACILLUS THURINGIENSIS	153-187					
CHILD NAME	19 KD INSECTICIDAL TOXIN	BACILLUS THURINGIENSIS	276-308					
CHILD NAME	19 KD INSECTICIDAL TOXIN	BACILLUS THURINGIENSIS	276-308					
CHILD NAME	19 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	207-234	232-279	429-463			
CHILD NAME	19 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	52-84	155-159	457-464			



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FCGENE	10/11/1914	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	Protein	
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PGENE	18111714	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PDHGP_BACNE	GLUCOSE 1-DEHYDROGENASE B	BACILLUS MEGATERIUM	275-27							
PDHGO_ECOLI	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	436-403							
PDHRI_STRVN	KETOACYL REDUCTASE I	STREPTOMYCES VIOLACEORUBER	188-195							
PDHLE_BACST	LEUCINE DEHYDROGENASE	BACILLUS STEAROTERMOPHILUS	192-219							
PDHLO_AGR12	P-LYSINE DEHYDROGENASE	AGROBACTERIUM TUMEFACIENS	312-344							
PDHMI_MBTX	METHANOL DEHYDROGENASE SUBUNIT I PAEC	METHYLOBACTERIUM EXTORQUENS	132-187	190-224						
PDHMI_MBTX	METHANOL DEHYDROGENASE SUBUNIT I PAEC	METHYLOBACTERIUM ORGANOPHILUM	153-187	190-224						
PDHMI_PARDI	METHANOL DEHYDROGENASE SUBUNIT I PAEC	PARACOCOCUS DENTIFICANS	193-232							
PDHNA_BACSP	NADH DEHYDROGENASE	BACILLUS SP	246-314							
PDHNA_ECOLI	NADH DEHYDROGENASE	ESCHERICHIA COLI	106-214							
PDHOM_BACSU	HOMOSERINE DEHYDROGENASE	BACILLUS SUBTILIS	72-107	408-433						
PDHOM_CORGL	HOMOSERINE DEHYDROGENASE	CORYNEBACTERIUM GLUTAMICUM	105-132							
PDHOM_BACSH	PHENYLALANINE DEHYDROGENASE	BACILLUS SPHAERICUS	212-239							
PDHRA_ECOLI	SUCC DEHYDROGENASE FLAVOPROTEIN SUBUNIT	ESCHERICHIA COLI	482-512							
PDHRS_ANACY	SOLUBLE HYDROGENASE 43 KD SUBUNIT	ANABAENA CYLINDRICA	86-113	110-168						
PDHRT_METHA	TRIMETHYLAMINE DEHYDROGENASE	STREPTOCOCCUS SP	123-160							
PDHRO_ECOLI	PROBABLE ATP-DEPENDENT HELICASE DING	METHYLOTROPHUS METHYLOPHILUS	439-466							
PDHVB_BACSU	DIVISION INITIATION PROTEIN	ESCHERICHIA COLI	364-411	114-141						
PDHVI_PSEPU	DITHYDROLIPOLAMIDE DEHYDROGENASE	BACILLUS SUBTILIS	54-82							
PDHVI_AZONI	LIPOLAMIDE DEHYDROGENASE COMPLEX (E1)	PSEUDOMONAS PUTIDA	91-120							
PDHVI_BACST	LIPOLAMIDE DEHYDROGENASE COMPLEX (E1)	AZOTOBACTER VINELANDII	18-45	224-276						
PDHVI_BACSU	LIPOLAMIDE DEHYDROGENASE COMPLEX (E2)	BACILLUS STEAROTERMOPHILUS	82-124							
PDHVI_ECOLI	DITHYDROLIPOLAMIDE DEHYDROGENASE	BACILLUS SUBTILIS	82-109							
PDHVI_PSEPU	DITHYDROLIPOLAMIDE DEHYDROGENASE	ESCHERICHIA COLI	108-133							
PDHVP_PSEPU	PHENOL HYDROXYLASE P1 PROTEIN	PSEUDOMONAS FLUORESCENS	124-151	223-235						
PDHVA_BACSU	DNAA PROTEIN	PSEUDOMONAS PUTIDA	61-90							
PDHVA_BACSU	DNAA PROTEIN	BACILLUS SUBTILIS	497-524	548-581						
PDHVA_BACSU	DNAA PROTEIN	BACILLUS SUBTILIS	456-483							
PDHVA_BACSU	DNAA PROTEIN	BACILLUS SUBTILIS	116-140							
PDHVA_BACSU	DNAA PROTEIN	BORRELLIA BURGDORFERI	182-216	248-273	341-387	416-463				
PDHVA_BACSU	DNAA PROTEIN	BORRELLIA AFRICAENSIS	32-100	111-118	353-310					
PDHVA_BACSU	DNAA PROTEIN	ESCHERICHIA COLI	186-200							
PDHVA_ECOLI	DNAA PROTEIN	MICROCOCCUS LUTEUS	183-415							
PDHVA_MICLU	DNAA PROTEIN	MYCOPLASMA CAPRICOLUM	8-36	73-112	274-310	350-389				
PDHVA_MYCCA	DNAA PROTEIN	PROTEUS MIRABILIS	163-199							
PDHVA_PSEPU	DNAA PROTEIN	PSEUDOMONAS PUTIDA	198-219							
PDHVA_PSEPU	DNAA PROTEIN	SPYROPLASMA CITRI	43-72	26-110	145-180					
PDHVA_PSEPU	DNAA PROTEIN	CLOSTRIDIUM TRACIONATIS	312-333							
PDHVA_PSEPU	DNAA PROTEIN	ESCHERICHIA COLI	82-109							
PDHVA_PSEPU	DNAA PROTEIN	SALMONELLA TYPHIMURUM	82-109							
PDHVA_PSEPU	DNAA PROTEIN	ESCHERICHIA COLI	166-190							
PDHVA_PSEPU	DNAA PROTEIN	ESCHERICHIA COLI	497-524	548-581						
PDHVA_PSEPU	DNAA PROTEIN	BORRELLIA BURGDORFERI	312-394							
PDHVA_PSEPU	DNAA PROTEIN	BRUCELLA OVIS	248-273	312-346						
PDHVA_PSEPU	DNAA PROTEIN	CAULOBACTERIA CRESCENTUS	161-188							
PDHVA_PSEPU	DNAA PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	499-526							
PDHVA_PSEPU	DNAA PROTEIN	CLOSTRIDIUM PERFRINGENS	498-527							
PDHVA_PSEPU	DNAA PROTEIN	METHANOCALDOCoccus MAZELI	513-550							
PDHVA_PSEPU	DNAA PROTEIN	MYCOBACTERIUM TUBERCULOSIS	502-539							
PDHVA_PSEPU	DNAA PROTEIN	STREPTOMYCES COELICOLOR	43-72	337-372						
PDHVA_PSEPU	DNAA PROTEIN	ESCHERICHIA COLI	114-141							
PDHVA_PSEPU	DNAA PROTEIN	ZYMONOMAS MOBILIS	638-712							
PDHVA_PSEPU	DNAA PROTEIN	STREPTOMYCES PELICULUS	24-31							
PDHVA_PSEPU	DNAA PROTEIN	SULFOLOBUS SOLFATILICUS	184-172							
PDHVA_PSEPU	DNAA PROTEIN	BACILLUS SUBTILIS	58-85	417-444	1382-1416					
PDHVA_PSEPU	DNAA PROTEIN	ESCHERICHIA COLI	77-104							
PDHVA_PSEPU	DNAA PROTEIN	SACCHAROPOLYSPORA ERYTHRAEA	210-237							



[illegible]



[illegible]



ECGENE	10111144	Protein Name	Protein Description	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ZIPK NAME	PROTEIN	PROTEIN	PROTEIN	22-56								
PF0001 STAAU	POSSIBLE PROTEIN FEMB	POSSIBLE PROTEIN FEMB	POSSIBLE PROTEIN FEMB	4-31								
PF0002 STN21	FERREDOXIN-NADP REDUCTASE	FERREDOXIN-NADP REDUCTASE	FERREDOXIN-NADP REDUCTASE	176-201								
PF0003 ECOLI	FERRIC ENTEROBACTIN TRANSPORT PROTEIN	FERRIC ENTEROBACTIN TRANSPORT PROTEIN	FERRIC ENTEROBACTIN TRANSPORT PROTEIN	182-234								
PF0004 ECOLI	FERRIC ENTEROBACTIN TRANSPORT PROTEIN	FERRIC ENTEROBACTIN TRANSPORT PROTEIN	FERRIC ENTEROBACTIN TRANSPORT PROTEIN	128-155								
PF0005 ECOLI	FERRIC ENTEROBACTIN TRANSPORT PROTEIN	FERRIC ENTEROBACTIN TRANSPORT PROTEIN	FERRIC ENTEROBACTIN TRANSPORT PROTEIN	2-39								
PF0006 ANASP	FERREDOXIN-NADP REDUCTASE	FERREDOXIN-NADP REDUCTASE	FERREDOXIN-NADP REDUCTASE	67-94								
PF0007 ANASP	FERREDOXIN-LIKE PROTEIN IN NIF REGION	FERREDOXIN-LIKE PROTEIN IN NIF REGION	FERREDOXIN-LIKE PROTEIN IN NIF REGION	1128-1138								
PF0008 BOPPE	FILAMENTOUS HEMAGGLUTININ	FILAMENTOUS HEMAGGLUTININ	FILAMENTOUS HEMAGGLUTININ	142-169								
PF0009 BOPPE	HADMOLEXYLINE-LIKE PROTEIN	HADMOLEXYLINE-LIKE PROTEIN	HADMOLEXYLINE-LIKE PROTEIN	16-63								
PF0010 ECOLI	FORMATE HYDROGENLYASE TRANSACTIVATOR	FORMATE HYDROGENLYASE TRANSACTIVATOR	FORMATE HYDROGENLYASE TRANSACTIVATOR	458-485								
PF0011 ECOLI	FERROCHROME-IRON RECEPTOR PRECURSOR	FERROCHROME-IRON RECEPTOR PRECURSOR	FERROCHROME-IRON RECEPTOR PRECURSOR	272-354								
PF0012 ECOLI	PROTEIN FIBRIN PRECURSOR	PROTEIN FIBRIN PRECURSOR	PROTEIN FIBRIN PRECURSOR	187-214								
PF0013 ECOLI	OUTER-MEMBRANE RECEPTOR	OUTER-MEMBRANE RECEPTOR	OUTER-MEMBRANE RECEPTOR	161-195								
PF0014 ECOLI	OUTER-MEMBRANE RECEPTOR	OUTER-MEMBRANE RECEPTOR	OUTER-MEMBRANE RECEPTOR	151-178								
PF0015 ECOLI	CELL FILAMENTATION PROTEIN	CELL FILAMENTATION PROTEIN	CELL FILAMENTATION PROTEIN	151-178								
PF0016 ECOLI	CELL FILAMENTATION PROTEIN	CELL FILAMENTATION PROTEIN	CELL FILAMENTATION PROTEIN	204-335								
PF0017 ECOLI	OUTER-MEMBRANE PROTEIN	OUTER-MEMBRANE PROTEIN	OUTER-MEMBRANE PROTEIN	51-78								
PF0018 ECOLI	CHAPERONE PROTEIN	CHAPERONE PROTEIN	CHAPERONE PROTEIN	222-353								
PF0019 ECOLI	FMAD PROTEIN PRECURSOR	FMAD PROTEIN PRECURSOR	FMAD PROTEIN PRECURSOR	165-192								
PF0020 ECOLI	TYPE 1 TUBULIN REGULATORY PROTEIN	TYPE 1 TUBULIN REGULATORY PROTEIN	TYPE 1 TUBULIN REGULATORY PROTEIN	49-76								
PF0021 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	41-69								
PF0022 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	175-209								
PF0023 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	145-172								
PF0024 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	162-189								
PF0025 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	129-156								
PF0026 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	242-274								
PF0027 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	27-54								
PF0028 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	83-92								
PF0029 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	28-73								
PF0030 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	36-63								
PF0031 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	15-76								
PF0032 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	36-90								
PF0033 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	36-63								
PF0034 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	73-149								
PF0035 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	15-42								
PF0036 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	226-364								
PF0037 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	18-42								
PF0038 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	1-41								
PF0039 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	181-219								
PF0040 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	162-189								
PF0041 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	51-49								
PF0042 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	242-270								
PF0043 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	144-191								
PF0044 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	270-364								
PF0045 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	86-113								
PF0046 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	18-52								
PF0047 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	291-318								
PF0048 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	102-129								
PF0049 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	63-49								
PF0050 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	12-30								
PF0051 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	81-105								
PF0052 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	81-105								
PF0053 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	6-33								
PF0054 ECOLI	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	FABRIAE 2 PROTEIN	198-232								



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ECGENE	1993/1994	Protein	Protein Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
ECGENE	1993/1994	Protein	Protein Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
PRDA1 ECOLI	PRDA1	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT	ORGANISMS	395-422											
PRDA2 ECOLI	PRDA2	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT	WOLINELLA SUCCINIGENES	6-35	487-514										
PRDA3 ECOLI	PRDA3	GLIDING MOTILITY REGULATORY PROTEIN	MYXOCOCCUS XANTHUS	15-42	478-505										
PRDA4 ECOLI	PRDA4	FORMATE-TETRAHYDROFOLATE LIGASE	CLOSTRIDIUM THERMOCETUM	161-190											
PRDA5 ECOLI	PRDA5	FORMATE-TETRAHYDROFOLATE LIGASE	METHANOBACTERIUM THERMOAUTOTROPHICUS	161-190											
PRDA6 ECOLI	PRDA6	CELL DIVISION PROTEIN FTSA	BACILLUS SUBTILIS	78-110											
PRDA7 ECOLI	PRDA7	CELL DIVISION PROTEIN FTSA	ESCHERICHIA COLI	301-318	375-418										
PRDA8 ECOLI	PRDA8	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	6-31											
PRDA9 ECOLI	PRDA9	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	61-90											
PRDA10 ECOLI	PRDA10	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	151-188											
PRDA11 ECOLI	PRDA11	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	278-305											
PRDA12 ECOLI	PRDA12	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	216-240											
PRDA13 ECOLI	PRDA13	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	7-41											
PRDA14 ECOLI	PRDA14	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	290-317											
PRDA15 ECOLI	PRDA15	CELL DIVISION PROTEIN FTSL	BACILLUS SUBTILIS	414-445											
PRDA16 ECOLI	PRDA16	CELL DIVISION PROTEIN FTSL	YERSINIA PESTIS	99-130											
PRDA17 ECOLI	PRDA17	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	302-329											
PRDA18 ECOLI	PRDA18	CELL DIVISION PROTEIN FTSL	ANABASNA VARIABILIS	83-114											
PRDA19 ECOLI	PRDA19	CELL DIVISION PROTEIN FTSL	ANABASNA VARIABILIS	162-189											
PRDA20 ECOLI	PRDA20	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	216-240											
PRDA21 ECOLI	PRDA21	CELL DIVISION PROTEIN FTSL	BACILLUS MEGATERIUM	49-76	217-271										
PRDA22 ECOLI	PRDA22	CELL DIVISION PROTEIN FTSL	BACILLUS SUBTILIS	49-76											
PRDA23 ECOLI	PRDA23	CELL DIVISION PROTEIN FTSL	PYROCOCCUS WOESSEI	219-286											
PRDA24 ECOLI	PRDA24	CELL DIVISION PROTEIN FTSL	THERMOTOGA MARITIMA	290-328											
PRDA25 ECOLI	PRDA25	CELL DIVISION PROTEIN FTSL	BACILLUS STEAROTHERMOPHILUS	101-143	241-268										
PRDA26 ECOLI	PRDA26	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	301-328											
PRDA27 ECOLI	PRDA27	CELL DIVISION PROTEIN FTSL	ZYMONOMAS MOBILIS	161-192											
PRDA28 ECOLI	PRDA28	CELL DIVISION PROTEIN FTSL	PSEUDOMONAS FLUORESCENS	178-205											
PRDA29 ECOLI	PRDA29	CELL DIVISION PROTEIN FTSL	SALMONELLA TYPHIMURUM	86-113											
PRDA30 ECOLI	PRDA30	CELL DIVISION PROTEIN FTSL	HADOPHILUS INFLUENZAE	124-158	218-269										
PRDA31 ECOLI	PRDA31	CELL DIVISION PROTEIN FTSL	LACTOBACILLUS HELVETICUS	304-318											
PRDA32 ECOLI	PRDA32	CELL DIVISION PROTEIN FTSL	SALMONELLA TYPHIMURUM	51-91											
PRDA33 ECOLI	PRDA33	CELL DIVISION PROTEIN FTSL	HADOPHILUS INFLUENZAE	182-209											
PRDA34 ECOLI	PRDA34	CELL DIVISION PROTEIN FTSL	PSEUDOMONAS FLUORESCENS	231-278											
PRDA35 ECOLI	PRDA35	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	78-105											
PRDA36 ECOLI	PRDA36	CELL DIVISION PROTEIN FTSL	PHOTOBACTERIUM LEHOGNATHI	197-227	246-273										
PRDA37 ECOLI	PRDA37	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	10-37											
PRDA38 ECOLI	PRDA38	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	216-246											
PRDA39 ECOLI	PRDA39	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	60-94											
PRDA40 ECOLI	PRDA40	CELL DIVISION PROTEIN FTSL	BACILLUS SUBTILIS	49-83	182-216	330-384									
PRDA41 ECOLI	PRDA41	CELL DIVISION PROTEIN FTSL	BACILLUS SUBTILIS	291-323											
PRDA42 ECOLI	PRDA42	CELL DIVISION PROTEIN FTSL	BACILLUS SUBTILIS	11-40											
PRDA43 ECOLI	PRDA43	CELL DIVISION PROTEIN FTSL	STAPHYLOCOCCUS HAEMOLYTICUS	6-33											
PRDA44 ECOLI	PRDA44	CELL DIVISION PROTEIN FTSL	STAPHYLOCOCCUS HAEMOLYTICUS	6-33											
PRDA45 ECOLI	PRDA45	CELL DIVISION PROTEIN FTSL	BACILLUS SUBTILIS	378-423											
PRDA46 ECOLI	PRDA46	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	531-568											
PRDA47 ECOLI	PRDA47	CELL DIVISION PROTEIN FTSL	PSEUDOMONAS PUTIDA	519-566											
PRDA48 ECOLI	PRDA48	CELL DIVISION PROTEIN FTSL	BACILLUS SUBTILIS	74-81											
PRDA49 ECOLI	PRDA49	CELL DIVISION PROTEIN FTSL	PSEUDOMONAS PUTIDA	231-252											
PRDA50 ECOLI	PRDA50	CELL DIVISION PROTEIN FTSL	SYNECHOCYSTIS SP	218-222											
PRDA51 ECOLI	PRDA51	CELL DIVISION PROTEIN FTSL	BACILLUS STEAROTHERMOPHILUS	26-79											
PRDA52 ECOLI	PRDA52	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	376-283											
PRDA53 ECOLI	PRDA53	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	114-141											
PRDA54 ECOLI	PRDA54	CELL DIVISION PROTEIN FTSL	SALMONELLA TYPHIMURUM	114-141											
PRDA55 ECOLI	PRDA55	CELL DIVISION PROTEIN FTSL	ESCHERICHIA COLI	209-243											
PRDA56 ECOLI	PRDA56	CELL DIVISION PROTEIN FTSL	METHANOCOCCUS THERMOLITHOTROPHICUS	54-85											



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Phylogenic Sequence											
PGCENE	1071174.4	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	XANTHOMONAS CAMPESSTRIS	210-357								
PGSPF XANCP	PROTEIN F	PSEUDOMONAS AERUGINOSA	10-39								
PGSPH P3EAE	PROTEIN H PRECURSOR	AEROMONAS HYDROPHILA	27-61								
PGSPH AENNY	PROTEIN I PRECURSOR	ERWINIA CAROTOVORA	14-61								
PGSPI EAWCA	PROTEIN I PRECURSOR	KLERSIELLA PNEUMONIAE	140-167								
PGSPK EAWCA	PROTEIN K	ERWINIA CAROTOVORA	28-35								
PGSPK EAWCH	PROTEIN K	ERWINIA CHRYSANTHEMI	28-35								
PGSPK EAWPI	PROTEIN K	KLERSIELLA PNEUMONIAE	22-99								
PGSPK P3EAE	PROTEIN K	PSEUDOMONAS AERUGINOSA	262-289								
PGSPK EAWCII	PROTEIN L	ERWINIA CHRYSANTHEMI	7-42	248-246	231-338						
PGSPH XANCP	PROTEIN L	XANTHOMONAS CAMPESSTRIS	38-73	297-324							
PGSPH EAWCA	PROTEIN M	ERWINIA CAROTOVORA	108-165								
PGSPD EAWCH	PROTEIN D PRECURSOR	ERWINIA CHRYSANTHEMI	319-362	448-435	546-573	637-684					
PGPFI STRDO	GLUCOSYLTRANSFERASE-1 PRECURSOR	STREPTOCOCCUS DOWNEI	42-69	212-239	464-491	1385-1416	1495-1529				
PGPFI STRDO	GLUCOSYLTRANSFERASE-1 PRECURSOR	STREPTOCOCCUS DOWNEI	171-198	206-211	458-485	1312-1412	1497-1514				
PGPFI STRAM	GLUCOSYLTRANSFERASE-3	STREPTOCOCCUS MUTANS	297-350								
PGPFI STRAM	GLUCOSYLTRANSFERASE-1 PRECURSOR	STREPTOCOCCUS MUTANS	42-93	110-137	161-188	198-246	313-347	592-627			
PGPFI STRAM	GLUCOSYLTRANSFERASE-3 PRECURSOR	STREPTOCOCCUS MUTANS	4-40	110-138	235-261	306-361	614-657				
PGPFI STRAM	GLUCOSYLTRANSFERASE-3 PRECURSOR	STREPTOCOCCUS DOWNEI	275-316	438-463	1281-1313						
PGPFI METTF	POSSIBLE G-T MISMATCHES REPAIR ENZYME	METHANOBACTERIUM THERMAUTOTRUNCUM	10-107	148-175							
PGPFI METTF	GAP SYNTHASE	BACILLUS SUBTILIS	314-348	399-436	478-503						
PGPFI EAWCII	GAP SYNTHASE	ESCHERICHIA COLI	105-132								
PGPFI BACCI	BETA-GLUCANASE PRECURSOR	BACILLUS CIRCULANS	164-191								
PGPFI BACCI	BETA-GLUCANASE PRECURSOR	BACILLUS LICHENIFORMIS	172-166								
PGPFI BACCI	BETA-GLUCANASE PRECURSOR	BACILLUS MAGERANS	126-166								
PGPFI BACCI	ENDOGLUCANASE A	BACILLUS SP	18-49								
PGPFI BACCI	ENDOGLUCANASE PRECURSOR	BACILLUS SUBTILIS	270-304	376-403							
PGPFI BACCI	ENDOGLUCANASE 1	BUTYRIVIBRIO FIBRISOLVENS	154-181	432-495							
PGPFI BACCI	ENDOGLUCANASE E-2 PRECURSOR	BACILLUS SUBTILIS	270-304								
PGPFI BACCI	ENDOGLUCANASE C PRECURSOR	THELAMONOSPORA FUSCA	203-228	348-378	293-363						
PGPFI BACCI	ENDOGLUCANASE PRECURSOR	BACILLUS SUBTILIS	270-304								
PGPFI BACCI	ENDOGLUCANASE 1 PRECURSOR	FIBROBACTER SUCCINOGENES	342-346								
PGPFI BACCI	ENDOGLUCANASE E-4 PRECURSOR	THELAMONOSPORA FUSCA	208-242								
PGPFI BACCI	ENDOGLUCANASE E-5 PRECURSOR	THELAMONOSPORA FUSCA	44-71								
PGPFI BACCI	ENDOGLUCANASE A PRECURSOR	BACILLUS LAUTUS	418-437	434-481							
PGPFI BACCI	ENDOGLUCANASE A PRECURSOR	CLOSTRIDIUM THERMOCELLUM	354-384								
PGPFI BACCI	ENDOGLUCANASE A PRECURSOR	PSEUDOMONAS FLUORESCENS	762-789								
PGPFI BACCI	ENDOGLUCANASE A	RUMINOCOCCUS ALBUS	394-431								
PGPFI BACCI	CELLULOXYLTRANSFERASE A	RUMINOCOCCUS FLAVIFACIENS	376-403								
PGPFI BACCI	ENDOGLUCANASE B PRECURSOR	BACILLUS LAUTUS	376-430								
PGPFI BACCI	ENDOGLUCANASE B	CALDOCELLUM SACCHAROLYTICUM	151-181	444-478							
PGPFI BACCI	ENDOGLUCANASE B PRECURSOR	CELLULOMONAS FIMI	366-393								
PGPFI BACCI	ENDOGLUCANASE B PRECURSOR	CLOSTRIDIUM CELLULOVORANS	144-171	266-300							
PGPFI BACCI	ENDOGLUCANASE B PRECURSOR	CLOSTRIDIUM THERMOCELLUM	314-341								
PGPFI BACCI	ENDOGLUCANASE C PRECURSOR	CELLULOMONAS FIMI	881-908								
PGPFI BACCI	ENDOGLUCANASE C PRECURSOR	PSEUDOMONAS FLUORESCENS	52-82								
PGPFI BACCI	ENDOGLUCANASE D PRECURSOR	CLOSTRIDIUM CELLULOLYTICUM	382-453								
PGPFI BACCI	ENDOGLUCANASE D PRECURSOR	CLOSTRIDIUM CELLULOLYTICUM	145-172	274-298							
PGPFI BACCI	ENDOGLUCANASE E PRECURSOR	CLOSTRIDIUM THERMOCELLUM	158-185	203-236							
PGPFI BACCI	ENDOGLUCANASE E PRECURSOR	CLOSTRIDIUM THERMOCELLUM	46-73	423-452							
PGPFI BACCI	ENDOGLUCANASE H PRECURSOR	ERWINIA CAROTOVORA	20-47	113-149							
PGPFI BACCI	MUTATIVE ENDOGLUCANASE X	CLOSTRIDIUM THERMOCELLUM	103-139								
PGPFI BACCI	ENDOGLUCANASE Z PRECURSOR	CLOSTRIDIUM THERMOCELLUM	296-326	322-349							
PGPFI BACCI	ENDOGLUCANASE	BACILLUS STEAROMANUS	198-233								
PGPFI BACCI	ENDOGLUCANASE PRECURSOR	BACILLUS SP	321-348								
PGPFI BACCI	ENDOGLUCANASE PRECURSOR	BACILLUS SP	198-239	301-328	633-664						



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FCG#	GENE	10/1/78/4	Prokaryotic Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
1	UTRANKE	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PIPA1 SHFL	60 KD ANTIGEN		SHIGELLA FLEXNERI	282-312								AREA2
PIPA2 SHFL	70 KD ANTIGEN		SHIGELLA FLEXNERI	91-116		417-475	394-410					
PIPA3 SHFL	80 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	28-55		71-109	400-507	322-356				
PIPA4 SHFL	82 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	28-55		71-109	400-507	322-356				
PIPA5 SHFL	84 KD MEMBRANE ANTIGEN		SHIGELLA DYSENTERIAE	21-57		113-161	271-300	214-278				
PIPA6 SHFL	86 KD MEMBRANE ANTIGEN		SHIGELLA DYSENTERIAE	21-57		113-161	271-300	214-278				
PIPA7 SHFL	88 KD MEMBRANE ANTIGEN		SHIGELLA DYSENTERIAE	21-57		113-161	271-300	214-278				
PIPA8 SHFL	90 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	47-86		201-210						
PIPA9 SHFL	92 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	47-86		201-210						
PIPA10 SHFL	94 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	175-202		239-246	291-310					
PIPA11 SHFL	96 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	175-202								
PIPA12 SHFL	98 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	52-97		143-171						
PIPA13 SHFL	100 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	118-112		212-219	316-377					
PIPA14 SHFL	102 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	87-97								
PIPA15 SHFL	104 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	167-194								
PIPA16 SHFL	106 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	86-113								
PIPA17 SHFL	108 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	6-37								
PIPA18 SHFL	110 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	132-149								
PIPA19 SHFL	112 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	16-111								
PIPA20 SHFL	114 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	115-142		197-224	333-380					
PIPA21 SHFL	116 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	109-143								
PIPA22 SHFL	118 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	182-210								
PIPA23 SHFL	120 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	186-210		533-552	559-593					
PIPA24 SHFL	122 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	61-95								
PIPA25 SHFL	124 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	143-170								
PIPA26 SHFL	126 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	188-215								
PIPA27 SHFL	128 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	186-213								
PIPA28 SHFL	130 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	89-98								
PIPA29 SHFL	132 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	69-96								
PIPA30 SHFL	134 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	70-97								
PIPA31 SHFL	136 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	128-153								
PIPA32 SHFL	138 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	169-196								
PIPA33 SHFL	140 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	7-34								
PIPA34 SHFL	142 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	163-189								
PIPA35 SHFL	144 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	49-76								
PIPA36 SHFL	146 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	52-79								
PIPA37 SHFL	148 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	12-39								
PIPA38 SHFL	150 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	228-255								
PIPA39 SHFL	152 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	112-148								
PIPA40 SHFL	154 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	312-374								
PIPA41 SHFL	156 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	9-64								
PIPA42 SHFL	158 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	26-60								
PIPA43 SHFL	160 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	56-83		282-310						
PIPA44 SHFL	162 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	290-317								
PIPA45 SHFL	164 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	9-36								
PIPA46 SHFL	166 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	195-229								
PIPA47 SHFL	168 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	2-29								
PIPA48 SHFL	170 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	2-32								
PIPA49 SHFL	172 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	194-210								
PIPA50 SHFL	174 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	62-89		181-415						
PIPA51 SHFL	176 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	337-364								
PIPA52 SHFL	178 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	132-159								
PIPA53 SHFL	180 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	171-198								
PIPA54 SHFL	182 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	44-71								
PIPA55 SHFL	184 KD MEMBRANE ANTIGEN		SHIGELLA FLEXNERI	162-189		207-234	311-333					



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GENE	1071714	Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PLUCASE	PROXIN	ALKANAL MONOOXYGENASE ALPHA CHAIN	190-217								
PLUKA KAYAL	KRYTOPHANALON	ALKANAL MONOOXYGENASE BETA CHAIN	184-217	237-291							
PLUXB PHOPO	ALCANAL MONOOXYGENASE BETA CHAIN	PHOTOBACTERIUM PHOSPHOREUM	184-217								
PLUXB VIBHA	ALCANAL MONOOXYGENASE BETA CHAIN	VIBRIO HARVEY	372-400								
PLUXC PHOLE	ACYL-COA REDUCTASE	PHOTOBACTERIUM LEONATHI	44-81								
PLUXC PHOPO	ACYL-COA REDUCTASE	PHOTOBACTERIUM PHOSPHOREUM	34-91								
PLUXC VIBFI	ACYL-COA REDUCTASE	VIBRIO FISCHERI	16-45								
PLUXC XENLU	ACYL-COA REDUCTASE	XENORHABDUS LUMINESCENS	39-49								
PLUXD PHOLE	ACYL TRANSFERASE	PHOTOBACTERIUM LEONATHI	89-119	218-245							
PLUXD VIBHA	LUCIFERIN-COMPONENT LIGASE	VIBRIO HARVEY	20-37								
PLUXD PHOLE	NON-FLUORESCENT FLAVOPROTEIN	PHOTOBACTERIUM LEONATHI	145-175	190-226							
PLUXD PHOPO	NON-FLUORESCENT FLAVOPROTEIN	PHOTOBACTERIUM PHOSPHOREUM	17-85								
PLUXG VIBFI	PROBABLE FLAVIN REDUCTASE	VIBRIO FISCHERI	137-168								
PLUXH VIBHA	LUXH PROTEIN	VIBRIO HARVEY	96-123								
PLUXI VIBFI	OHRL SYNTHESIS PROTEIN LUXI	VIBRIO FISCHERI	30-37								
PLUXJ VIBFI	OHRL SYNTHESIS PROTEIN LUXJ	VIBRIO FISCHERI	31-65	162-189							
PLUXP PHOMO	LUXAZINE PROTEIN	PHOTOBACTERIUM PHOSPHOREUM	81-88								
PLUXR VIBHA	LUXR REGULATORY PROTEIN	VIBRIO HARVEY	268-295								
PLXBI PHOLE	ALKANAL MONOOXYGENASE BETA CHAIN	PHOTOBACTERIUM LEONATHI	228-255								
PLXBI PHOLE	ALKANAL MONOOXYGENASE BETA CHAIN	PHOTOBACTERIUM LEONATHI	81-114								
PLXB BACSU	B-ENZYME	BACILLUS SUBTILIS	81-118								
PLYC CLOAB	AUTOLYTIC LYSOZYME	ESCHERICHIA COLI	142-176								
PLYB BACSU	AMIDASE EMIANCEA PRECURSOR	BACILLUS SUBTILIS	55-82	150-177	555-585						
PLYB ECOLI	LYTB PROTEIN	ESCHERICHIA COLI	210-237								
PLYC BACSU	AMIDASE PRECURSOR	BACILLUS SUBTILIS	179-213	225-252							
PLYTR BACSU	MEMBRANE-BOUND PROTEIN LYTR	BACILLUS SUBTILIS	13-64	259-303							
PNH1 STRPY	M PROTEIN, SEROTYPE 12 PRECURSOR	STREPTOCOCCUS PYOGENES	46-92	114-156	193-417	436-484					
PNH2 STRPY	M PROTEIN, SEROTYPE 24 PRECURSOR	STREPTOCOCCUS PYOGENES	12-48	89-118	245-272	280-313	399-437				
PNH3 STRPY	M PROTEIN, SEROTYPE 49 PRECURSOR	STREPTOCOCCUS PYOGENES	12-174	289-327							
PNH4 STRPY	M PROTEIN, SEROTYPE 5 PRECURSOR	STREPTOCOCCUS PYOGENES	5-39	56-263	306-333	351-410					
PNH5 STRPY	M PROTEIN, SEROTYPE 8 PRECURSOR	STREPTOCOCCUS PYOGENES	12-39	76-282	290-324	341-401					
PNH6 ECOLI	MALTOSE-BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	20-47								
PNH7 ENTAE	MALTOSE-BINDING PROTEIN PRECURSOR	ENTEROBACTER AEROGENES	30-47								
PNH8 ENTAE	INNER MEMBRANE PROTEIN MALX	ENTEROBACTER AEROGENES	3-30								
PNH9 STRPY	MALT REGULATORY PROTEIN	ESCHERICHIA COLI	832-879								
PNH10 STRPY	MALT PROTEIN PRECURSOR	STREPTOCOCCUS PNEUMONIAE	40-67	180-307							
PNH11 BACSM	1,4-BETA-MANNOSIDASE A AND B PREC	BACILLUS SP	410-441								
PNH12 CALSA	B-MANNANASE/ENDOGLUCANASE A PREC	CALDOCCELLUM SACCHARORUM YHICUM	339-423	592-626	1222-1254	1296-1322					
PNH13 BACST	MALATE OXIDOREDUCTASE	BACILLUS STUAROTII R4111TILUS	246-273								
PNH14 ECOLI	ANTIBIOTIC RESISTANCE PROTEIN MAAR	ESCHERICHIA COLI	95-122								
PNH15 ECOLI	MOBILIZATION PROTEIN MREB	ESCHERICHIA COLI	318-65	100-134							
PNH16 WOLNI	QUINONE-REDUCTASE/ITRICKINASE	WOLINELLA SUTCINOHENES	400-471								
PNH17 ECOLI	MCBB PROTEIN	ESCHERICHIA COLI	47-76	122-163							
PNH18 ECOLI	METHYL-ACCEPTING CHEMOTAXIS PROTEIN I	ESCHERICHIA COLI	172-206	228-255	306-345						
PNH19 ECOLI	METHYL-ACCEPTING CHEMOTAXIS PROTEIN II	ESCHERICHIA COLI	372-399								
PNH20 SALT	METHYL-ACCEPTING CHEMOTAXIS PROTEIN III	ESCHERICHIA COLI	238-306								
PNH21 ECOLI	METHYL-ACCEPTING CHEMOTAXIS PROTEIN IV	SALMONELLA TYPHIMURUM	238-306								
PNH22 ECOLI	METHYL-ACCEPTING CHEMOTAXIS PROTEIN V	ESCHERICHIA COLI	238-315								
PNH23 CANCR	CHEMOKINE RECEPTOR MCPA	ESCHERICHIA COLI	111-145	164-191	277-304						
PNH24 SALT	CHEMOTAXIS CITRATE TRANSDUCER	CALDOBACTER CRESCENTUS	260-287	369-403	516-543						
PNH25 ENTAE	CHEMOTAXIS ASPARTATE TRANSDUCER	SALMONELLA TYPHIMURUM	314-348								
PNH26 ENTAE	CHEMOTAXIS SERINE TRANSDUCER	ENTEROBACTER AEROGENES	275-303								
PNH27 ECOLI	SPECIFIC RESTRICTION ENZYME A	ENTEROBACTER AEROGENES	41-68	158-208	317-351	408-532					
PNH28 MEIRA	METHYL-COENZYME M REDUCTASE	ESCHERICHIA COLI	37-71								
PNH29 MEIRA	METHYL-COENZYME M REDUCTASE	METHANOSARCINA BARKEI	373-405								
PNH30 MEIRA	METHYL-COENZYME M REDUCTASE	METHANOCOCCUS VANNIELII	335-363								
PNH31 MEIRA	METHYL-COENZYME M REDUCTASE	METHANOCOCCUS VOLTAE	335-363								



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PCGENE	10117814	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
U1EMAMK	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PMAR2 KLEPN	EMBRIA ADHESIN PROTEIN PRECURSOR	KLEBSIELLA PNEUMONIAE	222-268								
PMAR3 KLEPN	MOLE PROTEIN	KLEBSIELLA PNEUMONIAE	193-220								
PMAR4 STRPY	FIBRINOGEN/710 BINDING PROTEIN PRECURSOR	STREPTOCOCCUS PYOGENES	7-46	99-210							
PMAR5 STRSU	MURAMIDASE-RELEASED PROTEIN PRECURSOR	STREPTOCOCCUS SUIS	75-102	110-177	261-291						
PMAR6 ECOLI	PROB ATP-BINDING TRANSPORT PROTEIN MSBA	ESCHERICHIA COLI	116-150	412-449							
PMAR7 STAEF	ERYTHROMYCIN RESISTANCE PROTEIN	STAPHYLOCOCCUS EPIDERMIDIS	174-223	322-350							
PMAR8 ECOLI	ACIDIC PROTEIN MSYB	ESCHERICHIA COLI	71-100								
PMAR9 ECOLI	MODIFICATION METHYLASE ECO37I	ESCHERICHIA COLI	250-284	474-544							
PMAR10 ACICA	MODIFICATION METHYLASE ACCI	ACINETOBACTER CALCOACECTICUS	503-540								
PMAR11 SYN2P	MODIFICATION METHYLASE ACUI RETA SUBUNIT	SYNECHOCOCCUS SP	19-46								
PMAR12 BREP	MODIFICATION METHYLASE BEPI	BREVIBACTERIUM EPIDERMIDIS	166-200	309-336							
PMAR13 HERAU	MODIFICATION METHYLASE HOBI	HERPETOSSIPHON AURANTIACUS	281-308								
PMAR14 BACAM	MODIFICATION METHYLASE BAMBII	BACILLUS AMYLOLIQUEFACIENS	35-42								
PMAR15 BACAR	MODIFICATION METHYLASE BANII	BACILLUS ANEURINOLYTICUS	184-211								
PMAR16 BACSU	MODIFICATION METHYLASE BSUBI	BACILLUS ANEURINOLYTICUS	121-148	382-409							
PMAR17 BACSU	MODIFICATION METHYLASE BSUBI	BACILLUS SUBTILIS	231-258	467-496							
PMAR18 CITR	MODIFICATION METHYLASE CTRBI	BACILLUS SUBTILIS	208-235								
PMAR19 HERAU	MODIFICATION METHYLASE HOCI	CITROBACTER FREUNDII	2-36	55-82	332-379						
PMAR20 HERAU	MODIFICATION METHYLASE HOCI	HERPETOSSIPHON AURANTIACUS	120-147								
PMAR21 ECOLI	MODIFICATION METHYLASE ECOLI	ESCHERICHIA COLI	281-311								
PMAR22 ECOLI	MODIFICATION METHYLASE HOCI	ESCHERICHIA COLI	76-110	145-172							
PMAR23 ECOLI	MODIFICATION METHYLASE HOCI	HERPETOSSIPHON AURANTIACUS	281-308								
PMAR24 ECOLI	MODIFICATION METHYLASE ECO RV	ESCHERICHIA COLI	4-61								
PMAR25 ENTCL	MODIFICATION METHYLASE ECJ	ENTEROBACTER CLOACAE	32-100								
PMAR26 FLAOK	MODIFICATION METHYLASE FOKI	FLAVOBACTERIUM OREANOKOITES	418-445								
PMAR27 FUSNU	MODIFICATION METHYLASE FNUH	FUSOBACTERIUM NUCLEATUM	184-211	276-306	337-366	398-425	555-646				
PMAR28 HAEGA	MODIFICATION METHYLASE HGA2	HAEMOPHILUS GALLINARUM	72-49								
PMAR29 HAEN	MODIFICATION METHYLASE HNCI	HAEMOPHILUS INFLUENZAE	155-163								
PMAR30 METTF	MODIFICATION METHYLASE MTHCI	METHANOBACTERIUM THERMOFORMICICUM	181-208	199-226							
PMAR31 KLEPN	MODIFICATION METHYLASE KPN	KLEBSIELLA PNEUMONIAE	181-215	196-221							
PMAR32 STRMU	MODIFICATION METHYLASE MTHCI	STREPTOCOCCUS MUTANS	320-297								
PMAR33 MOXSP	MODIFICATION METHYLASE MSHI	MORAXELLA SP	39-66	224-251	349-376						
PMAR34 NEILA	MODIFICATION METHYLASE NLAII	NEISSERIA LACTAMICA	5-39	48-104							
PMAR35 PROVU	MODIFICATION METHYLASE PVU II	PROTEUS VULGARIS	124-158	183-210							
PMAR36 SULAC	MEMBRANE-ASSOCIATED ATPASE	SULFOLOBUS ACIDOCALDIARIUS	308-335								
PMAR37 PROST	MODIFICATION METHYLASE PSTI	PROVIDENCIA STUARTII	9-47								
PMAR38 ECOLI	TAT/TOPHAM-SPECIFIC TRANSPORT PROTEIN	ESCHERICHIA COLI	226-264								
PMAR39 STRSA	MODIFICATION METHYLASE STSI	STREPTOCOCCUS SANGUIS	80-107								
PMAR40 SHISO	MODIFICATION METHYLASE SHOI	SHIGELLA SONNEI	116-153	434-461	600-645						
PMAR41 STAAU	MODIFICATION METHYLASE SAU6I	STAPHYLOCOCCUS AUREUS	81-108								
PMAR42 LACLC	MODIFICATION METHYLASE SCRF-A	LACTOCOCCUS LACTIS	333-274								
PMAR43 SPISO	MODIFICATION METHYLASE SCRF-B	LACTOCOCCUS LACTIS	84-115	187-214							
PMAR44 SERMA	CPG DNA METHYLASE	STREPTOCOCCUS MUTANS	27-41								
PMAR45 TRETII	MODIFICATION METHYLASE SMAI	SPHILOPLASMA SP	118-230	236-290							
PMAR46 VIBSI	MODIFICATION METHYLASE VSP	SERRATIA MARCESCENS	61-88								
PMAR47 ECOLI	MODIFICATION METHYLASE VSP	THERMUS AQUATICUS	130-157								
PMAR48 ERWAM	MAJOR OUTER MEMBRANE LIPOPROTEIN PREC	VIBRIO SP	33-66								
PMAR49 MO	MAJOR OUTER MEMBRANE LIPOPROTEIN PREC	ESCHERICHIA COLI	330-381	1014-1048	1216-1232						
PMAR50 PROBI	MAJOR OUTER MEMBRANE LIPOPROTEIN PREC	ERWINIA AMYLOVORA	24-54								
PMAR51 BAFSU	UDP-LIGASE	MORAXELLA MORGANII	21-54								
PMAR52 ECOLI	UDP-MURNAAC-PENTAPEPTIDE SYNTHETASE	PROTEUS MIRABILIS	31-43								
PMAR53 ECOLI	ENOLPYRUVATE TRANSFERASE	BACILLUS SUBTILIS	101-132	299-326							
PMAR54 ENTCL	ENOLPYRUVATE TRANSFERASE	ESCHERICHIA COLI	107-134								
PMAR55 STRCH	METHYLMALONYL-COA MUTASE BETA-SUBUNIT	ESCHERICHIA COLI	392-419								
		ENTEROBACTER CLOACAE	392-419								
		STREPTOMYCES CARMANONENSIS	31-58								



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PCGNAME	10717845	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
FILENAME	ZROLEN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															



GENE	1971-1974	Proteolytic Sequence	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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PCGENE	10711714	Prokaryotic Sequences	ORGANISM	ARLAL	ARLAL	ARLAL	ARLAL	ARLAL	ARLAL
FILEMANIE	PROTEIN		ANACYSTIS NIDULANS	99-126	209-241				
PP3B0 ANANI	STABILIZING POLYPEPTIDE PRECURSOR		ESCHERICHIA COLI	55-52					
PP3B0 ECOLI	SHAGE SICK PROTEIN A		WOLINELLA SUCCINIMENTS	114-111					
PP3B0 WOLSU	POLYGLUTAMIDE REINFORCE CHAIN A PRECURSOR		ESCHERICHIA COLI	40-74					
PP3B5 ECOLI	PHOSPHATE-BINDING PROTEIN PRECURSOR		BACILLUS SUBTILIS	28-60					
PP3B5 BACSU	PHOSPHOTRANSFERASE		ESCHERICHIA COLI	135-162	199-428				
PP3B5 ECOLI	PHOSPHOTRANSFERASE		SALMONELLA TYPHIMURUM	322-259	199-428				
PP3B5 STACTY	PHOSPHOTRANSFERASE		STAPHYLOCOCCUS CARNOSEUS	34-61	191-232				
PP3B5 STACTA	PHOSPHOTRANSFERASE		STREPTOCOCCUS SALIVARIUS	34-61	127-154				
PP3B5 STREL	PHOSPHOTRANSFERASE ENZYME II		ERWINIA CHRYSANTHEMI	670-697					
PP3B5 BACSU	PHOSPHOTRANSFERASE ENZYME II		BACILLUS SUBTILIS	137-364					
PP3B5 LACCA	PHOSPHOTRANSFERASE ENZYME II		LACTOCOCCUS LACTIS	103-214	609-438				
PP3B5 LACCA	PHOSPHOTRANSFERASE ENZYME II		STAPHYLOCOCCUS ALTEUS	421-448	330-553				
PP3B5 STAAU	PHOSPHOTRANSFERASE ENZYME II		ESCHERICHIA COLI	445-489					
PP3B5 ECOLI	PHOSPHOTRANSFERASE ENZYME II		STAPHYLOCOCCUS CARNOSEUS	388-415					
PP3B5 STACA	PHOSPHOTRANSFERASE ENZYME II		ESCHERICHIA COLI	370-400					
PP3B5 ECOLI	N-ACETYLGLUCOSAMINE PHENYLASE		STREPTOCOCCUS MUTANS	600-637					
PP3B5 STANU	PHOSPHOTRANSFERASE ENZYME II		SALMONELLA TYPHIMURUM	107-124					
PP3B5 SALTY	PHOSPHOTRANSFERASE FPM PROTEIN		LACTOBACILLUS CASEI	40-67					
PP3B5 LACCA	PHOSPHOTRANSFERASE FACTOR III		ESCHERICHIA COLI	11-65					
PP3B5 ECOLI	PHOSPHOCARBON PROTEIN HPA		SALMONELLA TYPHIMURUM	31-65					
PP3B5 KLEPN	PHOSPHOCARBON PROTEIN HPA		KLEBSIELLA PNEUMONIAE	94-121	217-231				
PP3B5 ECOLI	PROTEASE II		ESCHERICHIA COLI	894-928					
PP3B5 KLEAE	PULLULANASE		KLEBSIELLA AEROGES	894-918					
PP3B5 KLEPN	PULLULANASE		KLEBSIELLA PNEUMONIAE	178-205					
PP3B5 KLEPN	LEADER PEPTIDASE		KLEBSIELLA PNEUMONIAE	70-97					
PP3B5 KLEPN	PULS PRECURSOR		KLEBSIELLA PNEUMONIAE	112-162	479-46	716-761			
PP3B5 PSEPU	UPTAKE PROTEIN PRECURSOR		PSEUDOMONAS PUTIDA	384-421					
PP3B5 BACSU	AMIDOPHOSPHORIBOSYL TRANSFERASE		BACILLUS SUBTILIS	349-376					
PP3B5 BACSU	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE		BACILLUS SUBTILIS	149-176					
PP3B5 BACSU	FORMYLTRANSFERASE		BACILLUS SUBTILIS	23-34					
PP3B5 ECOLI	FORMYLTRANSFERASE		ESCHERICHIA COLI	18-45					
PP3B5 BACSU	SYNTHASE I		BACILLUS SUBTILIS	153-194					
PP3B5 BACSU	CYCLO-LIGASE		ESCHERICHIA COLI	131-158					
PP3B5 ECOLI	AIR CARBOXYLASE		BACILLUS SUBTILIS	3-43					
PP3B5 BACSU	SARCAR SYNTHETASE		BACILLUS SUBTILIS	56-120	326-333				
PP3B5 BACSU	ADENYLOSUCINATE LYASE		ESCHERICHIA COLI	184-221	321-372				
PP3B5 ECOLI	ADENYLOSUCINATE LYASE		BACILLUS SUBTILIS	18-33	345-372				
PP3B5 BACSU	AICAR TRANSFORMYLASE		BACILLUS SUBTILIS	239-268					
PP3B5 ECOLI	AICAR TRANSFORMYLASE		ESCHERICHIA COLI	218-247					
PP3B5 SALTY	AICAR TRANSFORMYLASE		SALMONELLA TYPHIMURUM	609-616					
PP3B5 BACSU	SYNTHASE II		BACILLUS SUBTILIS	88-113					
PP3B5 ANASP	LINKER POLYPEPTIDE CPCGI		ANABAENA SP	89-116					
PP3B5 MASLA	LINKER POLYPEPTIDE CPCGI		MASTIGOCALDUS LAMINOSUS	88-115					
PP3B5 ANASP	LINKER POLYPEPTIDE CPCGI		ANABAENA SP	89-116					
PP3B5 MASLA	LINKER POLYPEPTIDE CPCGI		MASTIGOCALDUS LAMINOSUS	91-132					
PP3B5 MASLA	LINKER POLYPEPTIDE CPCGI		MASTIGOCALDUS LAMINOSUS	90-131					
PP3B5 ANASP	LINKER POLYPEPTIDE CPCGI		ANABAENA SP	33-42					
PP3B5 ANASP	321 KD LINKER POLYPEPTIDE		ANABAENA SP	105-112					
PP3B5 FREDI	379 KD LINKER POLYPEPTIDE		FREMYELLA DIPLOSPHON	32-46					
PP3B5 FREDI	314 KD LINKER POLYPEPTIDE		FREMYELLA DIPLOSPHON	108-143					
PP3B5 FREDI	373 KD LINKER POLYPEPTIDE		FREMYELLA DIPLOSPHON	43-70	111-140				
PP3B5 FREDI	308 KD LINKER POLYPEPTIDE		FREMYELLA DIPLOSPHON	9-36					
PP3B5 BACSU	ASPARTATE CARBAMOYLTRANSFERASE		BACILLUS SUBTILIS	70-97					
PP3B5 SERMA	ASPARTATE CARBAMOYLTRANSFERASE		SERATIA MARCESCENS	115-142					
PP3B5 ECOLI	ORITHIDROATE DEHYDROGENASE		ESCHERICHIA COLI						



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ECGENE	1071784	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PRM1 STAP	REPLICATION AND MAINTENANCE PROTEIN	STAPHYLOCOCCUS EPIDERMIDIS	81-108						
PRFP ECOLI	REPLICATION PROTEIN REPA	ESCHERICHIA COLI	36-77						
PRFA BACSU	REPA PROTEIN	BACILLUS SUBTILIS	163-373						
PRFA ECOLI	REPA PROTEIN	ESCHERICHIA COLI	91-118						
PRFA NEG0	REPLICATION PROTEIN	NEISSERIA GONORRHOEAE	57-84						
PRFB LACPL	REPLICATION PROTEIN REPD	LACTOBACILLUS PLANTARUM	184-211						
PRFM STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	354-384						
PRFN STAAU	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	258-285						
PRFA STAG	REPR PROTEIN	STREPTOCOCCUS AGALACTIAE	430-467						
PRFS STAP	REPS PROTEIN	STREPTOCOCCUS PYOGENES	423-467						
PRFX STAAU	REP PROTEIN	STAPHYLOCOCCUS AUREUS	111-150						
PRFP ECOLI	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	288-315						
PRFP ECOLI	REPLICATION PROTEIN	CLOSTRIDIUM PERFRINGENS	164-195	393-324					
PRFP ECOLI	REP HELICASE	ESCHERICHIA COLI	119-146	205-243					
PRFP ECOLI	REP PROTEIN	LACTOBACILLUS PLANTARUM	119-199	240-287					
PRFP CLOPE	RESOLVASE	CLOSTRIDIUM PERFRINGENS	68-103	151-185					
PRF3 BACSU	PROBABLE PEPTIDE CHAIN RELEASE FACTOR 2	BACILLUS SUBTILIS	34-68						
PRF3 ECOLI	PEPTIDE CHAIN RELEASE FACTOR 3	ESCHERICHIA COLI	16-113	163-204					
PRF3 SALT	PEPTIDE CHAIN RELEASE FACTOR 2	SALMONELLA TYPHIMURUM	16-113	163-204					
PRF3 ECOLI	PEPTIDE CHAIN RELEASE FACTOR 3	ESCHERICHIA COLI	180-210	443-473					
PRFA ECOLI	1,4-GALACTOSYLTRANSFERASE	ESCHERICHIA COLI	189-226						
PRFA ECOLI	BIOSYNTHESIS PROTEIN NPAG	ESCHERICHIA COLI	185-212						
PRFA ECOLI	1,3-GLUCOSYLTRANSFERASE	ESCHERICHIA COLI	59-66	233-264					
PRFA ECOLI	1,2-GLUCOSYLTRANSFERASE	SALMONELLA TYPHIMURUM	145-172	216-263					
PRFA SALT	1,2-N-ACETYLGLUCOSAMINETRANSFERASE	SALMONELLA TYPHIMURUM	333-369						
PRFA ECOLI	O-ANTIGEN LIASE	ESCHERICHIA COLI	166-193						
PRFA SALT	O-ANTIGEN LIASE	SALMONELLA TYPHIMURUM	326-360						
PRFA ECOLI	BIOSYNTHESIS PROTEIN NPAP	ESCHERICHIA COLI	8-23						
PRFA ECOLI	BIOSYNTHESIS PROTEIN NPAS	ESCHERICHIA COLI	62-89	184-240					
PRFA ECOLI	BIOSYNTHESIS PROTEIN NPAY	ESCHERICHIA COLI	18-45						
PRFA ECOLI	BIOSYNTHESIS PROTEIN NPZ	ESCHERICHIA COLI	3-20	93-112					
PRFB SALT	OTDP-GLUCOSE 4,6-DEHYDRATASE	SALMONELLA TYPHIMURUM	330-359						
PRFB SALT	MANNOSYL-1-PHOSPHATE GUANYLYLTRANSFERASE	SALMONELLA TYPHIMURUM	333-361						
PRFB SALT	PARATOSE SYNTHASE	VIBRIO ANGUILLARUM	349-376						
PRFA VIBAN	PRECURSOR FOR FERREIC ANGUILLIBACTIN	SALMONELLA TYPHIMURUM	83-110						
PRFB ECOLI	PEPTIDE CHAIN RELEASE FACTOR HOMOLOG	ESCHERICHIA COLI	22-56	203-232					
PRFB ECOLI	PUTATIVE G12 SITE-SPECIFIC RECOMBINASE	BACILLUS THURINGIENSIS	15-48	190-163					
PRFA ECOLI	DHAPULOXINASE	ESCHERICHIA COLI	135-202						
PRFA SALT	DHAPULOXINASE	SALMONELLA TYPHIMURUM	175-202						
PRFA ECOLI	L-RHAMNOSE OPERON TRANSACTIVATOR	ESCHERICHIA COLI	10-41						
PRFA ECOLI	L-RHAMNOSE OPERON REG PROTEIN RHAS	ESCHERICHIA COLI	132-179						
PRFA ECOLI	RHIR REGULATORY PROTEIN	RHIZOBIUM LEGUMINOSARUM	206-233						
PRFB ECOLI	RNA HELICASE RHLBACRA	ESCHERICHIA COLI	118-165						
PRFB ECOLI	TRANS TERNITACTOR RHO	BORDELLIA BURGDORFERI	215-242	327-369					
PRFB ECOLI	PROTEASE PROD REG PROTEIN IIPA	BACILLUS SUBTILIS	82-109						
PRFA BACSU	RHSA PROTEIN PRECURSOR	ESCHERICHIA COLI	667-694						
PRFA ECOLI	RHSA PROTEIN PRECURSOR	ESCHERICHIA COLI	300-418	667-694					
PRFA ECOLI	RHSC PROTEIN PRECURSOR	ESCHERICHIA COLI	671-712	1071-1098					
PRFA ECOLI	RHSD PROTEIN PRECURSOR	ESCHERICHIA COLI	393-372						
PRFA ECOLI	RHSE PROTEIN	ESCHERICHIA COLI	93-127						
PRFA ECOLI	ACETYLTRANSFERASE	ESCHERICHIA COLI	167-194						
PRFA ECOLI	RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE	PHOTOBACTERIUM LEIOGNATHI	2-47	131-158					
PRFA ECOLI	RIBOFLAVIN SYNTHASE ALPHA CHAIN	BACILLUS SUBTILIS	8-33						
PRFB BACSU	RIBOFLAVIN SYNTHASE BETA CHAIN	PHOTOBACTERIUM LEIOGNATHI	14-41						
PRFB ECOLI	RIBOFLAVIN SYNTHASE BETA CHAIN	PHOTOBACTERIUM LEIOGNATHI	14-41						
PRFA STAP	MS RIBOSOMAL PROTEIN L10	STREPTOCOCCUS ANTIDITHIOTICUS	14-22	106-133					
PRFA STAP	MS RIBOSOMAL PROTEIN L12	STREPTOCOCCUS ANTIDITHIOTICUS	2-34						



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FCG:ENE	107:117:14	Proteins: Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILEMANIC	PROTEIN	ORGANISMS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PIAT1 TREPA	41 KD MEMBRANE ANTIGEN PRECURSOR	TREPONEMA PALLIDUM	28-33									
PIAT2 TREDE	51 KD MEMBRANE ANTIGEN A PRECURSOR	TREPONEMA DENTICOLA	99-126	291-329								
PIAT3 BACAL	ALVEOLYIN PRECURSOR	BACILLUS ALVEI	373-381	374-401								
PIAT4 CLOFE	PENFUNGOLYIN PRECURSOR	CLOSTRIDIUM PERFRINGENS	376-381	377-434								
PIAT5 LISIV	IVANOLYIN PRECURSOR	LISTERIA IVANOVII	91-120	167-195	196-433							
PIAT6 LISMO	LISTERIOLYIN O PRECURSOR	LISTERIA MONOCYTOGENES	91-125	168-196	197-424							
PIAT7 LISSE	SEELIGEROLYIN PRECURSOR	LISTERIA SEELIGER	99-126	296-323	349-376	399-463						
PIAT8 STRPN	PNEUMOLYIN	STREPTOCOCCUS PNEUMONIAE	314-373									
PIAT9 STRPY	STREPTOLYIN O PRECURSOR	STREPTOCOCCUS PYOGENES	86-133	335-382	440-470							
PIAG1 BACSU	TECHNOIC ACID BIOSYN PROTEIN B PREC	BACILLUS SUBTILIS	42-49									
PIAG2 BACSU	TECHNOIC ACID BIOSYNTHESIS PROTEIN C	BACILLUS SUBTILIS	248-375									
PIAG3 BACSU	TECHNOIC ACID BIOSYNTHESIS PROTEIN E	BACILLUS SUBTILIS	59-92	164-181	185-243	565-592	600-637					
PIAG4 BACSU	TECHNOIC ACID BIOSYNTHESIS PROTEIN F	BACILLUS SUBTILIS	182-209									
PIAG5 BACSU	TECHNOIC ACID BIOSYNTHESIS PROTEIN G	BACILLUS SUBTILIS	19-21	117-164	198-433	810-841						
PIB11 NEGO	TRANSFERRIN-BINDING PROTEIN I PRECURSOR	NEISSERIA GONORRHOEA	18-43	227-234	375-402							
PIB12 NEGO	PHENOL 2-MONOOXYGENASE	PSEUDOMONAS PICKETTII	105-132									
PTC01 DALTY	TRANSCRIPTIONAL REGULATORY PROTEIN TCDT	SALMONELLA TYPHIMURUM	20-47	83-128	199-233	263-290	344-375	459-486				
PTCPC VIBCH	NEBRIANE PROTEIN TPCP PRECURSOR	VIBRIO CHOLERAE	24-39	77-111								
PTCPE VIBCH	TCP PILUS BIOSYNTHESIS PROTEIN TCFE	VIBRIO CHOLERAE	32-46	311-318								
PTCPE VIBCH	TCP PILUS SECRETION PROTEIN TCFE	VIBRIO CHOLERAE	95-122									
PTCPE VIBCH	TCP PILUS BIOSYNTHESIS PROTEIN TCFH	VIBRIO CHOLERAE	35-52	234-261	279-306	346-379						
PTCPE VIBCH	TCP PILUS BIOSYNTHESIS PROTEIN TCFI	VIBRIO CHOLERAE	48-75									
PTCPE VIBCH	TCP PILUS VIRULENCE REGULATORY PROTEIN	VIBRIO CHOLERAE	121-148									
PTCPE VIBCH	TCP PILUS BIOSYNTHESIS PROTEIN TCF2	VIBRIO CHOLERAE	44-45									
PTCPE VIBCH	TCP PILUS BIOSYNTHESIS PROTEIN TCF3	VIBRIO CHOLERAE	404-434									
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN	BACILLUS STEAROTHERMOPHILUS	422-453									
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN	STAPHYLOCOCCUS AUREUS	404-431									
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN	STREPTOCOCCUS AGALACTIAE	422-453									
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN	STREPTOCOCCUS PNEUMONIAE	422-453									
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN	ESCHERICHIA COLI	210-239									
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN	ESCHERICHIA COLI	374-361									
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN	STREPTOCOCCUS PYOGENES	177-164	161-393	400-437							
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN	ESCHERICHIA COLI	8-16									
PTCPE VIBCH	TETRAACYCLINE REPRESSOR PROTEIN CLASS B	ESCHERICHIA COLI	183-210									
PTCPE VIBCH	TETRAACYCLINE REPRESSOR PROTEIN CLASS D	ESCHERICHIA COLI	41-86									
PTCPE VIBCH	TETRAACYCLINE REPRESSOR PROTEIN TERA	ALCALIGENES SP	4-31									
PTCPE VIBCH	ACTYL-COA THIOESTERASE II	ESCHERICHIA COLI	2-36	136-139	179-206	217-244						
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN TETM	ENTEROCOCCUS FAECALIS	2-36	136-139	179-206	217-244						
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN TETM	ENTEROCOCCUS FAECALIS	2-36	136-139	179-206	217-244						
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN TETM	ESCHERICHIA COLI	32-108	116-138								
PTCPE VIBCH	TRANSPOSIN T101 TETC PROTEIN	ESCHERICHIA COLI	92-109									
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN	STREPTOCOCCUS LIVIDANS	2-36	136-139	217-244	260-287						
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN TETM	UREAPLASMA UREALYTICUM	2-36									
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN TETM	CAMPYLOBACTER COLI	2-36									
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN TETM	CAMPYLOBACTER REDUJI	2-36									
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN TETM	STREPTOCOCCUS MUTANS	2-36									
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN TETM	STREPTOCOCCUS MUTANS	2-36									
PTCPE VIBCH	TETRAACYCLINE RESISTANCE PROTEIN	BACTERIOIDES FRAGILIS	35-42									
PTCPE VIBCH	TETANUS TOXIN PRECURSOR	CLOSTRIDIUM TETANI	374-304	340-367	613-642	692-719	913-1012	1240-1277				
PTCPE VIBCH	TRANS INITIATION FACTOR IID IONOMOLOG	PROCOCCUS WORSEI	218-238									
PTCPE VIBCH	CHLOROACETOL 1,2-DIOXYGENASE	ALCALIGENES EUTROPHUS	2-37									
PTCPE VIBCH	QUELONINE TRNA-RIBOSYLTRANSFERASE	ESCHERICHIA COLI	173-200									
PTCPE VIBCH	THREONINE DEHYDROXYLASE BIOSYNTHETIC	LACTOCOCCUS LACTIS	267-303									
PTCPE VIBCH	THREONINE DEHYDROXYLASE BIOSYNTHETIC	ESCHERICHIA COLI	293-320									
PTCPE VIBCH	THREONINE DEHYDROXYLASE BIOSYNTHETIC	BACILLUS SUBTILIS	133-180	192-216	282-316	391-418						
PTCPE VIBCH	FURAN OXIDATION PROTEIN THOF	ESCHERICHIA COLI	226-260	404-431								
PTCPE VIBCH	FURAN OXIDATION PROTEIN THOF	PSEUDOMONAS PUTIDA	4-18	240-267								
PTCPE VIBCH	THEMOLYIN	BACILLUS CEREUS	45-72									
PTCPE VIBCH	THEMOLYIN PRECURSOR	BACILLUS STEAROTHERMOPHILUS	45-72									



FCGNE	101174.4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PT181 BACTH	THERMOLYSIN	BACILLUS THERMOPROTEOLYTICUS	86-113						
PT182 THEVU	THERMOLYSIN	ESCHERICHIA COLI	332-343	301-328					
PT183 ECOLI	THIC PROTEIN	ESCHERICHIA COLI	138-165						
PT184 ECOLI	THIC PROTEIN	ESCHERICHIA COLI	135-172	199-213					
PT185 SULAC	THERMOPHILIN PRECURSOR	SULFOLOBUS ACIDOCALDARIUS	288-315						
PT186 BUELA	THREONINE SYNTHASE	BREVI BACTERIUM LACTOFERMENTUM	69-96						
PT187 SACER	PURATIVE THIOSULFATE SULFUR TRANSFERASE	SACCHAROPOLYSPORA ERYTHRAEA	144-171						
PT188 ECOLI	TRIGGER FACTOR	ESCHERICHIA COLI	226-266						
PT189 TREPA	TREPONEMAL MEMBRANE PROTEIN A PRECURSOR	TREPONEMA PALLIDUM	44-71						
PT190 TREPA	TREPONEMAL MEMBRANE PROTEIN B PRECURSOR	TREPONEMA PALLIDUM	41-68						
PT191 TREPH	TREPONEMAL MEMBRANE PROTEIN C PRECURSOR	TREPONEMA PHAGEDENS	74-108						
PT192 ECOLI	LOW AFFINITY TRYPTOPHAN PERMEASE	ESCHERICHIA COLI	52-79	332-349					
PT193 STAAU	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	59-97	111-138					
PT194 STAAU	TRANSPOSASE A	STAPHYLOCOCCUS AUREUS	131-178						
PT195 STAAU	TRANSPOSASE B	STAPHYLOCOCCUS AUREUS	359-625						
PT196 BACTU	TNP1 RESOLVASE	BACILLUS THURINGIENSIS	742	61-92	174-201				
PT197 ECOLI	TRANSPOSIN TNP1 TRANSPOSITION PROTEIN TNSB	ESCHERICHIA COLI	98-126	510-537					
PT198 ECOLI	TRANSPOSIN TNP1 TRANSPOSITION PROTEIN TNSC	ESCHERICHIA COLI	12-39	314-341					
PT199 ECOLI	TRANSPOSIN TNP1 TRANSPOSITION PROTEIN TNSD	ESCHERICHIA COLI	339-366						
PT200 ECOLI	TRANSPOSIN TNP1 TRANSPOSITION PROTEIN TNSE	ESCHERICHIA COLI	461-490						
PT201 PSEPU	TOLUENE 1,2-DIOXYGENASE ALPHA SUBUNIT	PSEUDOMONAS PUTIDA	36-63						
PT202 PSEPU	TOLUENE 1,2-DIOXYGENASE BETA SUBUNIT	PSEUDOMONAS PUTIDA	119-133						
PT203 PSEPU	TOLUENE 1,2-DIOXYGENASE SYSTEM	PSEUDOMONAS PUTIDA	179-213						
PT204 PSEPU	TODP PRODUCT HYDROLASE	PSEUDOMONAS PUTIDA	143-170						
PT205 ECOLI	TOLA PROTEIN	ESCHERICHIA COLI	101-138						
PT206 ECOLI	OUTER MEMBRANE PROTEIN TOLC PRECURSOR	ESCHERICHIA COLI	144-178	184-211	313-443				
PT207 STNPT	DNA TOPOISOMERASE I	SYNECHOCOCCUS SP	203-230						
PT208 ECOLI	TRIMETHYLAMINE-N-OXIDE REDUCTASE	ESCHERICHIA COLI	197-224						
PT209 BORPE	PERTUSSIS TOXIN SUBUNIT 1 (S1) PRECURSOR	BORDETELLA PERTUSSIS	179-206						
PT210 BORPE	PERTUSSIS TOXIN SUBUNIT 2 (S2) PRECURSOR	BORDETELLA PERTUSSIS	38-65						
PT211 CLODI	TOXIN A	CLOSTRIDIUM DIFFICILE	20-81	99-159	204-231	142-269	373-414	847-963	997-1024
PT212 PEAB	EXOTOXIN A PRECURSOR	PSEUDOMONAS AERUGINOSA	479-497						
PT213 CLODI	TOXIN B	CLOSTRIDIUM DIFFICILE	38-72	133-163	199-241	815-869	922-950	1334-1388	1403-1433
PT214 VBCH	TRANSMEMBRANE REGULATORY PROTEIN TOX3	VIBRIO CHOLERAE	13-40						
PT215 TREPA	ANTIGEN TPF1	TREPONEMA PALLIDUM	106-143						
PT216 ECOLI	TRIOSEPHOSPHATE ISOMERASE	ESCHERICHIA COLI	81-110						
PT217 MORSP	TRIOSEPHOSPHATE ISOMERASE	MORAXELLA SP	119-164						
PT218 PORCI	THIOL PROTEIN PRECURSOR	PORPHYROMONAS GINGIVALIS	117-144						
PT219 AGRT3	TRYPTOPHAN 2-MONOOXYGENASE	AGROBACTERIUM TUMEFACIENS	219-268	581-529					
PT220 AGRT4	TRYPTOPHAN 2-MONOOXYGENASE	AGROBACTERIUM TUMEFACIENS	219-268	581-529					
PT221 PSESS	TRYPTOPHAN 2-MONOOXYGENASE	PSEUDOMONAS SYRINGAE	41-68						
PT222 STAAU	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	38-113						
PT223 STAAU	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	11-31	58-113					
PT224 ECOLI	TRANSPOSASE	ESCHERICHIA COLI	721-735						
PT225 RHME	TRANSPOSASE	RHOBIUM MELLITI	179-206						
PT226 STAAU	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	33-40	68-95					
PT227 ECOLI	TRANSPOSASE	ESCHERICHIA COLI	181-208	308-340	710-734				
PT228 ECOLI	TRANSPOSASE	ESCHERICHIA COLI	51-78						
PT229 SHRO	TRANSPOSASE	SHIGELLA SONNEI	51-78	200-227	231-258				
PT230 ECOLI	TRANSPOSASE	ESCHERICHIA COLI	729-756						
PT231 MYCTU	PURATIVE TRANSPOSASE	MYCOBACTERIUM TUBERCULOSIS	159-186						
PT232 BACTB	IS21B PROBABLE TRANSPOSASE	BACILLUS THURINGIENSIS	281-308	419-446					
PT233 BACTB	IS21C PROBABLE TRANSPOSASE	BACILLUS THURINGIENSIS	281-308	419-446					
PT234 STAAU	TRANSPOSASE	STAPHYLOCOCCUS AUREUS	4-31	45-72					
PT235 BACTB	IS21D PROBABLE TRANSPOSASE	BACILLUS THURINGIENSIS	281-308	419-446					
PT236 BACTU	TRANSPOSASE	BACILLUS THURINGIENSIS	93-127	509-539					



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[illegible]



TCGEME	10/21/2016	Phylogenetic Sequences	ORFAL	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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234	AREA1235	AREA1236	AREA1237	AREA1238	AREA1239	AREA1240	AREA1241	AREA1242	AREA1243	AREA1244	AREA1245	AREA1246	AREA1247	AREA1248	AREA1249	AREA1250	AREA1251	AREA1252	AREA1253	AREA1254	AREA1255	AREA1256	AREA1257	AREA1258	AREA1259	AREA1260	AREA1261	AREA1262	AREA1263	AREA1264	AREA1265	AREA1266	AREA1267	AREA1268	AREA1269	AREA1270	AREA1271	AREA1272	AREA1273	AREA1274	AREA1275	AREA1276	AREA1277	AREA1278	AREA1279	AREA1280	AREA1281	AREA1282	AREA1283	AREA1284	AREA1285	AREA1286	AREA1287	AREA1288	AREA1289	AREA1290	AREA1291	AREA1292	AREA1293	AREA1294	AREA1295	AREA1296	AREA1297	AREA1298	AREA1299	AREA1300	AREA1301	AREA1302	AREA1303	AREA1304	AREA1305	AREA1306	AREA1307	AREA1308	AREA1309	AREA1310	AREA1311	AREA1312	AREA1313	AREA1314	AREA1315	AREA1316	AREA1317	AREA1318	AREA1319	AREA1320	AREA1321	AREA1322	AREA1323	AREA1324	AREA1325	AREA1326	AREA1327	AREA1328	AREA1329	AREA1330	AREA1331	AREA1332	AREA1333	AREA1334	AREA1335	AREA1336	AREA1337	AREA1338	AREA1339	AREA1340	AREA1341	AREA1342	AREA1343	AREA1344	AREA1345	AREA13
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GENE	1071284	Protein Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PROTIN	1071284	PROTIN	70-97						
PROTIN	1071284	PROTIN	101-170						
PROTIN	1071284	PROTIN	172-159						
PROTIN	1071284	PROTIN	404-413						
PROTIN	1071284	PROTIN	172-149						
PROTIN	1071284	PROTIN	70-103						
PROTIN	1071284	PROTIN	270-347						
PROTIN	1071284	PROTIN	34-74						
PROTIN	1071284	PROTIN	46-113	182-209	273-304				
PROTIN	1071284	PROTIN	56-83						
PROTIN	1071284	PROTIN	2-39						
PROTIN	1071284	PROTIN	61-97						
PROTIN	1071284	PROTIN	221-248						
PROTIN	1071284	PROTIN	30-38	270-297					
PROTIN	1071284	PROTIN	22-87						
PROTIN	1071284	PROTIN	16-120						
PROTIN	1071284	PROTIN	293-327						
PROTIN	1071284	PROTIN	51-78						
PROTIN	1071284	PROTIN	33-105						
PROTIN	1071284	PROTIN	201-242	310-407					
PROTIN	1071284	PROTIN	51-92						
PROTIN	1071284	PROTIN	130-134						
PROTIN	1071284	PROTIN	203-214						
PROTIN	1071284	PROTIN	61-94						
PROTIN	1071284	PROTIN	172-200						
PROTIN	1071284	PROTIN	132-159						
PROTIN	1071284	PROTIN	13-40						
PROTIN	1071284	PROTIN	28-55						
PROTIN	1071284	PROTIN	272-306						
PROTIN	1071284	PROTIN	112-139						
PROTIN	1071284	PROTIN	6-31						
PROTIN	1071284	PROTIN	83-110	120-134	297-324				
PROTIN	1071284	PROTIN	612-646						
PROTIN	1071284	PROTIN	333-384						
PROTIN	1071284	PROTIN	72-99						
PROTIN	1071284	PROTIN	9-36						
PROTIN	1071284	PROTIN	6-33						
PROTIN	1071284	PROTIN	22-63						
PROTIN	1071284	PROTIN	18-71						
PROTIN	1071284	PROTIN	136-163						
PROTIN	1071284	PROTIN	225-263						
PROTIN	1071284	PROTIN	26-53						
PROTIN	1071284	PROTIN	214-241						
PROTIN	1071284	PROTIN	110-137	419-446					
PROTIN	1071284	PROTIN	7-34						
PROTIN	1071284	PROTIN	62-89						
PROTIN	1071284	PROTIN	123-152						
PROTIN	1071284	PROTIN	66-100						
PROTIN	1071284	PROTIN	312-339						
PROTIN	1071284	PROTIN	31-78						
PROTIN	1071284	PROTIN	84-122						
PROTIN	1071284	PROTIN	81-120						
PROTIN	1071284	PROTIN	30-57						
PROTIN	1071284	PROTIN	112-149						
PROTIN	1071284	PROTIN	2-39						
PROTIN	1071284	PROTIN	38-65	414-441	431-492				



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PCGENE	total/164	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
ELKNAME	PROTEIN	ORGANISM							
PT17 ACRI4	HYPOTHETICAL PROTEIN 7	AGROBACTERIUM TUMEFACIENS	20-56						
PT43 LEGIN	HYPOTHETICAL PROTEIN	LEGIONELLA PNEUMOPHILA	94-133						
PT45 BACAN	HYPOTHETICAL 31.8 KD PROTEIN	ENTEROCOCCUS FAECALIS	78-108						
PT47 ECOLI	HYPOTHETICAL 37.6 KD PROTEIN	BACILLUS ANTHRAKIS	13-47	115-162					
PT48 BACSU	HYPOTHETICAL 37.1 KD PROTEIN	ESCHERICHIA COLI	5-27						
PT49 ECOLI	HYPOTHETICAL 32.8 KD PROTEIN	BACILLUS SUBTILIS	184-222						
PT51 STN72	HYPOTHETICAL 18.1 KD PROTEIN	ESCHERICHIA COLI	16-43						
PT53 CLOPE	HYPOTHETICAL 19.7 KD PROTEIN	SYNECHOCOCCUS SP	34-61						
PT55 CLOPE	HYPOTHETICAL 14.3 KD PROTEIN	CLOSTRIDIUM PERFRINGENS	7-24	43-77	81-149				
PT57 CLOPE	HYPOTHETICAL 38.4 KD PROTEIN	CLOSTRIDIUM PERFRINGENS	2-59						
PT59 PSEAE	HYPOTHETICAL 38.3 KD PROTEIN	CLOSTRIDIUM PERFRINGENS	110-137	263-290	303-340				
PT61 BACSU	HYPOTHETICAL PROCESSING PROTEASE	PSUDOMONAS AERUGINOSA	22-52						
PT63 KLEPN	HYPOTHETICAL PROTEIN	BACILLUS SUBTILIS	329-356						
PT65 PLEBO	HYPOTHETICAL 31.1 KD PROTEIN	KLEBSIELLA PNEUMONIAE	243-270						
PT67 METF	HYPOTHETICAL 40.7 KD PROTEIN	PLECTONEMA BORYANUM	27-54						
PT69 METF	HYPOTHETICAL 23.3 KD PROTEIN	METHANOBACTERIUM THERMAUTOPHILICUM	58-85	308-335					
PT71 METF	HYPOTHETICAL 17.3 KD PROTEIN	METHANOBACTERIUM THERMAUTOPHILICUM	3-30						
PT73 METF	HYPOTHETICAL 49.6 KD PROTEIN	METHANOBACTERIUM THERMAUTOPHILICUM	69-117						
PT75 BACSU	HYPOTHETICAL 72.4 KD PROTEIN	BACILLUS SUBTILIS	333-360	389-430					
PT77 METF	HYPOTHETICAL 40.6 KD PROTEIN	METHANOBACTERIUM THERMAUTOPHILICUM	602-636						
PT79 METF	HYPOTHETICAL 31.1 KD PROTEIN	METHANOBACTERIUM THERMAUTOPHILICUM	58-85	308-335					
PT81 METF	HYPOTHETICAL 54.1 KD PROTEIN	METHANOBACTERIUM THERMAUTOPHILICUM	193-220	154-188					
PT83 METF	HYPOTHETICAL 9.7 KD PROTEIN	METHANOBACTERIUM THERMAUTOPHILICUM	226-253	381-408					
PT85 THE78	HYPOTHETICAL 18.7 KD PROTEIN	THEMOTILUM PUDENS	5-78						
PT87 HALCU	HYPOTHETICAL 40 KD GTP-BINDING PROTEIN	HALOBACTERIUM CUTIRUBUM	82-109						
PT89 SYN22	HYPOTHETICAL 28.7 KD PROTEIN	SYNECHOCOCCUS SP	20-51						
PT91 SALT	HYPOTHETICAL 40.6 KD PROTEIN	SALMONELLA TYPHIMURUM	49-76						
PT93 SALT	HYPOTHETICAL 51.0 KD PROTEIN	SALMONELLA TYPHIMURUM	103-190						
PT95 SALT	HYPOTHETICAL 20.6 KD PROTEIN	SALMONELLA TYPHIMURUM	428-455						
PT97 SALT	HYPOTHETICAL 34.6 KD PROTEIN	SALMONELLA TYPHIMURUM	39-56						
PT99 LACLA	HYPOTHETICAL PROTEIN	LACTOCOCCUS LACTIS	130-137						
PT101 METVA	HYPOTHETICAL PROTEIN	METHANOCOCCUS VANNIELII	140-167						
PT103 METVA	HYPOTHETICAL 11.6 KD PROTEIN	METHANOCOCCUS VANNIELII	40-93	129-156					
PT105 SULAC	HYPOTHETICAL 11.3 KD PROTEIN	SULFOLOBUS ACIDOCALDARIUS	12-40						
PT107 BACSU	HYPOTHETICAL 34.3 KD PROTEIN	SULFOLOBUS ACIDOCALDARIUS	3-51						
PT109 BACSU	HYPOTHETICAL 31.3 KD PROTEIN	BACILLUS SUBTILIS	37-71						
PT111 YEREN	HYPOTHETICAL 11.4 KD PROTEIN	BACILLUS SUBTILIS	39-56						
PT113 YEREN	HYPOTHETICAL YSC OPERON PROTEIN B	YERSINIA ENTEROCOLITICA	3-30	44-81					
PT115 YEREN	HYPOTHETICAL YSC OPERON PROTEIN C	YERSINIA ENTEROCOLITICA	90-121						
PT117 YEREN	HYPOTHETICAL YSC OPERON PROTEIN D	YERSINIA ENTEROCOLITICA	38-72	165-199					
PT119 YEREN	HYPOTHETICAL YSC OPERON PROTEIN H	YERSINIA ENTEROCOLITICA	242-269						
PT121 YEREN	HYPOTHETICAL YSC OPERON PROTEIN I	YERSINIA ENTEROCOLITICA	28-58						
PT123 YEREN	HYPOTHETICAL YSC OPERON PROTEIN L	YERSINIA ENTEROCOLITICA	49-76						
PT125 YEREN	HYPOTHETICAL YSC OPERON PROTEIN I PRECURSOR	YERSINIA PSEUDOTUBERCULOSIS	49-76						
PT127 YEREN	HYPOTHETICAL YSC OPERON PROTEIN I PRECURSOR	YERSINIA PSEUDOTUBERCULOSIS	99-126						
PT129 YEREN	HYPOTHETICAL YSC OPERON PROTEIN L	YERSINIA PSEUDOTUBERCULOSIS	99-126						
PT131 YEREN	HYPOTHETICAL YSC OPERON PROTEIN L	YERSINIA PSEUDOTUBERCULOSIS	41-48						
PT133 YEREN	HYPOTHETICAL 9.3 KD PROTEIN	SERRATIA MARCESCENS	11-70						
PT135 DESAM	HYPOTHETICAL 28.3 KD PROTEIN	DESULFURIBACILLUS AMBIVALENS	68-109						
PT137 DESAM	HYPOTHETICAL PROTEIN	DESULFURIBACILLUS AMBIVALENS	63-155						
PT139 LEPT	HYPOTHETICAL PROTEIN	LEPTOSPIRA INTERROGANS	6-33	60-94					
PT141 MYCAY	HYPOTHETICAL PROTEIN	MYCOPLASMA MYCOIDES	35-99	105-227	300-327				
PT143 BACSU	HYPOTHETICAL 19.6 KD PROTEIN	BACILLUS SUBTILIS	72-99						
PT145 METF	HYPOTHETICAL PROTEIN	METHANOTHERMICUS FERVIDUS	78-105						
PT147 STRFR	HYPOTHETICAL 37.1 KD PROTEIN	STREPTOMYCES FRADIAE	246-273						



PCGENE	10/11/14	Proteins Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN										
PTDR BACSU	HYPOTHETICAL 33.6 KD PROTEIN	DEGARDUSI	240-271	279-306							
PTDR LEPN	HYPOTHETICAL 33 KD PROTEIN	BACILLUS SUBTILIS	84-113								
PTDR LACLA	HYPOTHETICAL 13.3 KD PROTEIN	LEPTOSPIDA BIFLEXA	76-112								
PTDR BACSU	HYPOTHETICAL 70 KD PROTEIN	LACTOCOCCUS LACTIS	37-64								
PTDR SPICI	HYPOTHETICAL 23.8 KD PROTEIN	BACILLUS SUBTILIS	102-149								
PTDR BACSU	HYPOTHETICAL 23.8 KD PROTEIN	SPHIROPLASMA CITRI	37-64	63-93							
PTDR BACSU	HYPOTHETICAL 21.0 KD PROTEIN	BACILLUS SUBTILIS	142-169								
PTDR BACSU	HYPOTHETICAL 26.0 KD PROTEIN	BACILLUS SUBTILIS	17-31								
PTDR BACSU	HYPOTHETICAL 61.8 KD PROTEIN	BACILLUS SUBTILIS	163-207	263-289							
PTDR BACSU	HYPOTHETICAL 66.8 KD PROTEIN	BACILLUS SUBTILIS	3-30	34-61	94-143						
PTDR BACSU	HYPOTHETICAL 33.3 KD PROTEIN	BACILLUS SUBTILIS	36-83	113-112							
PTDR BACSU	HYPOTHETICAL 33.3 KD PROTEIN	BACILLUS SUBTILIS	24-38								
PTDR ANASP	HYPOTHETICAL 18.9 KD PROTEIN	ANABAEANA SP	27-104								
PTDR CALSA	HYPOTHETICAL 10.7 KD PROTEIN	CALDOCELLUM SACCHAROLYTICUM	8-39								
PTDR ECOLI	HYPOTHETICAL 14.7 KD PROTEIN	ESCHERICHIA COLI	41-94								
			91-78								



TABLE IX

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL HUMAN PROTEINS



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PROTEIN	INITIAL AND MAMM Search on All Human Protein Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7
PROLIN	NON-ERYTHROID PROTEIN 41 (BAND 41, LYMPHOCYTE FORM)	1-30						
P412 HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	172-200	518-545					
P42 HUMAN	4F3 CELL SURFACE ANTIGEN HEAVY CHAIN (F3HC) (LYMPHOCYTE ACTIVATION)	311-332						
P416 HUMAN	5-HYDROXYTRYPTAMINE 1E RECEPTOR (5-HT-1E) (SEROTONIN RECEPTOR)	311-338						
P417 HUMAN	5-HYDROXYTRYPTAMINE 1F RECEPTOR (5-HT-1F) (SEROTONIN RECEPTOR)	222-253						
P418 HUMAN	5-HYDROXYTRYPTAMINE 1A RECEPTOR (5-HT-1A) (SEROTONIN RECEPTOR)	32-36						
P419 HUMAN	5-HYDROXYTRYPTAMINE 1 RECEPTOR (5-HT-1) (5-HT-1X) (SEROTONIN RECEPTOR)	32-36						
P420 HUMAN	ALPHA-1-ANTITRYPSIN PRECURSOR (ACT)	98-132	310-337					
P421 HUMAN	ALPHA-1-ACID GLYCOPROTEIN 1 PRECURSOR (OROSOMUCOID) (OND)	92-119						
P422 HUMAN	ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1)	168-202						
P423 HUMAN	ALPHA-1-ANTITRYPSIN-RELATED PROTEIN PRECURSOR	161-197						
P424 HUMAN	ALPHA-3-ANTITRYPSIN PRECURSOR (ALPHA-3 PLASMIN INHIBITOR) (ALPHA-3)	191-218	165-195					
P425 HUMAN	LEUCINE-RICH ALPHA-3 GLYCOPROTEIN (LRG)	104-134						
P426 HUMAN	ALPHA-3-MACROGLOBULIN PRECURSOR (ALPHA-3-M)	51-80	119-149	103-1112	140-179			
P427 HUMAN	ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II)	428-453						
P428 HUMAN	ALPHA-ACTININ (F-ACTIN CROSS-LINKING PROTEIN)	92-119	720-747					
P429 HUMAN	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.1)	109-136						
P430 HUMAN	SMOOTH MUSCLE ACTIN-BINDING PROTEIN (ADP-360) (NONMUSCLE TILAKIN)	81-88	119-147	2604-1633				
P431 HUMAN	ACTIVATOR 1 17 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT) (A1)	306-333						
P432 HUMAN	ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (A1)	14-31	182-209	648-700				
P433 HUMAN	ACTYL-CoA DEHYDROGENASE PRECURSOR, LONG-CHAIN SPECIFIC (EC 1.9.9.13)	78-108	179-206	311-340				
P434 HUMAN	ANGIOTENSIN-CONVERTING ENZYME PRECURSOR, TESTIS-SPECIFIC (EC 1.4.15.1)	78-115	176-153	676-710				
P435 HUMAN	ANGIOTENSIN-CONVERTING ENZYME PRECURSOR, SOMATIC (EC 1.4.15.1) (ACE)	632-689	700-727	1750-1284				
P436 HUMAN	ACETYLCHOLINE RECEPTOR PROTEIN, EPSILON CHAIN PRECURSOR	48-80						
P437 HUMAN	ACE-TYLOSOLINE RECEPTOR PROTEIN, GAMMA CHAIN PRECURSOR	41-79	104-131					
P438 HUMAN	ACETYLCHOLINE RECEPTOR PROTEIN, BETA-4 CHAIN (BAGHENT)	39-56	70-97					
P439 HUMAN	ACETYLCHOLINE RECEPTOR (EC 1.2.1.10)	122-149						
P440 HUMAN	ACTIN PRECURSOR (EC 1.2.1.10)	26-33						
P441 HUMAN	ACTYLPHOSPHATASE, MUSCLE TYPE ISOZYME (EC 3.6.1.7) (ACTYLPHOSPHATE)	182-189						
P442 HUMAN	ADP-ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)	182-190						
P443 HUMAN	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM 1 (ADP/ATP TRANSLOCASE 3)	182-190						
P444 HUMAN	ALKALINE ANCHOR PROTEIN 78 (AKAP 78) (CAMP-DEPENDENT PROTEIN KINASE)	192-238	381-414					
P445 HUMAN	FRUCTOSE-BISPHOSPHATE ALDOLASE (EC 4.1.2.12) (A) (MUSCLE)	36-63						
P446 HUMAN	FRUCTOSE-BISPHOSPHATE ALDOLASE (EC 4.1.2.12) (B) (LIVER)	79-113						
P447 HUMAN	ADP DEAMINASE 1 (EC 3.5.4.6) (MYOADENYLATE DEAMINASE) (ADP DEAMINASE)	59-86						
P448 HUMAN	ADP DEAMINASE 2 (EC 3.5.4.6) (ADP DEAMINASE ISOFORM E)	69-76						
P449 HUMAN	ADENOPETIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (CPI150)	492-533	604-648	936-944				
P450 HUMAN	ADPHOSPHOLIPIN PRECURSOR (AA)	315-287						
P451 HUMAN	ALPHA-3-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR	173-236	263-290					
P452 HUMAN	BRAIN NATRIURETIC PEPTIDE PRECURSOR	36-63						
P453 HUMAN	ANKYRIN 1 (ANKYRIN 2.1 AND 2.3) (ERYTHROCYTE ANKYRIN)	1544-1571	1004-1031	1617-1644				
P454 HUMAN	ANKYRIN 2 (ANKYRIN 2.1 AND 2.3) (ERYTHROCYTE ANKYRIN)	1544-1571						
P455 HUMAN	ANKYRIN 3 (ANKYRIN 3.1 AND 3.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P456 HUMAN	ANKYRIN 4 (ANKYRIN 4.1 AND 4.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P457 HUMAN	ANKYRIN 5 (ANKYRIN 5.1 AND 5.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P458 HUMAN	ANKYRIN 6 (ANKYRIN 6.1 AND 6.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P459 HUMAN	ANKYRIN 7 (ANKYRIN 7.1 AND 7.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P460 HUMAN	ANKYRIN 8 (ANKYRIN 8.1 AND 8.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P461 HUMAN	ANKYRIN 9 (ANKYRIN 9.1 AND 9.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P462 HUMAN	ANKYRIN 10 (ANKYRIN 10.1 AND 10.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P463 HUMAN	ANKYRIN 11 (ANKYRIN 11.1 AND 11.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P464 HUMAN	ANKYRIN 12 (ANKYRIN 12.1 AND 12.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P465 HUMAN	ANKYRIN 13 (ANKYRIN 13.1 AND 13.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P466 HUMAN	ANKYRIN 14 (ANKYRIN 14.1 AND 14.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P467 HUMAN	ANKYRIN 15 (ANKYRIN 15.1 AND 15.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P468 HUMAN	ANKYRIN 16 (ANKYRIN 16.1 AND 16.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P469 HUMAN	ANKYRIN 17 (ANKYRIN 17.1 AND 17.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P470 HUMAN	ANKYRIN 18 (ANKYRIN 18.1 AND 18.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P471 HUMAN	ANKYRIN 19 (ANKYRIN 19.1 AND 19.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P472 HUMAN	ANKYRIN 20 (ANKYRIN 20.1 AND 20.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P473 HUMAN	ANKYRIN 21 (ANKYRIN 21.1 AND 21.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P474 HUMAN	ANKYRIN 22 (ANKYRIN 22.1 AND 22.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P475 HUMAN	ANKYRIN 23 (ANKYRIN 23.1 AND 23.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P476 HUMAN	ANKYRIN 24 (ANKYRIN 24.1 AND 24.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P477 HUMAN	ANKYRIN 25 (ANKYRIN 25.1 AND 25.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P478 HUMAN	ANKYRIN 26 (ANKYRIN 26.1 AND 26.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P479 HUMAN	ANKYRIN 27 (ANKYRIN 27.1 AND 27.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P480 HUMAN	ANKYRIN 28 (ANKYRIN 28.1 AND 28.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P481 HUMAN	ANKYRIN 29 (ANKYRIN 29.1 AND 29.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P482 HUMAN	ANKYRIN 30 (ANKYRIN 30.1 AND 30.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P483 HUMAN	ANKYRIN 31 (ANKYRIN 31.1 AND 31.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P484 HUMAN	ANKYRIN 32 (ANKYRIN 32.1 AND 32.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P485 HUMAN	ANKYRIN 33 (ANKYRIN 33.1 AND 33.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P486 HUMAN	ANKYRIN 34 (ANKYRIN 34.1 AND 34.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P487 HUMAN	ANKYRIN 35 (ANKYRIN 35.1 AND 35.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P488 HUMAN	ANKYRIN 36 (ANKYRIN 36.1 AND 36.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P489 HUMAN	ANKYRIN 37 (ANKYRIN 37.1 AND 37.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P490 HUMAN	ANKYRIN 38 (ANKYRIN 38.1 AND 38.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P491 HUMAN	ANKYRIN 39 (ANKYRIN 39.1 AND 39.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P492 HUMAN	ANKYRIN 40 (ANKYRIN 40.1 AND 40.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P493 HUMAN	ANKYRIN 41 (ANKYRIN 41.1 AND 41.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P494 HUMAN	ANKYRIN 42 (ANKYRIN 42.1 AND 42.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P495 HUMAN	ANKYRIN 43 (ANKYRIN 43.1 AND 43.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P496 HUMAN	ANKYRIN 44 (ANKYRIN 44.1 AND 44.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P497 HUMAN	ANKYRIN 45 (ANKYRIN 45.1 AND 45.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P498 HUMAN	ANKYRIN 46 (ANKYRIN 46.1 AND 46.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P499 HUMAN	ANKYRIN 47 (ANKYRIN 47.1 AND 47.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P500 HUMAN	ANKYRIN 48 (ANKYRIN 48.1 AND 48.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P501 HUMAN	ANKYRIN 49 (ANKYRIN 49.1 AND 49.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P502 HUMAN	ANKYRIN 50 (ANKYRIN 50.1 AND 50.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P503 HUMAN	ANKYRIN 51 (ANKYRIN 51.1 AND 51.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P504 HUMAN	ANKYRIN 52 (ANKYRIN 52.1 AND 52.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P505 HUMAN	ANKYRIN 53 (ANKYRIN 53.1 AND 53.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P506 HUMAN	ANKYRIN 54 (ANKYRIN 54.1 AND 54.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P507 HUMAN	ANKYRIN 55 (ANKYRIN 55.1 AND 55.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P508 HUMAN	ANKYRIN 56 (ANKYRIN 56.1 AND 56.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P509 HUMAN	ANKYRIN 57 (ANKYRIN 57.1 AND 57.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P510 HUMAN	ANKYRIN 58 (ANKYRIN 58.1 AND 58.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P511 HUMAN	ANKYRIN 59 (ANKYRIN 59.1 AND 59.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P512 HUMAN	ANKYRIN 60 (ANKYRIN 60.1 AND 60.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P513 HUMAN	ANKYRIN 61 (ANKYRIN 61.1 AND 61.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P514 HUMAN	ANKYRIN 62 (ANKYRIN 62.1 AND 62.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P515 HUMAN	ANKYRIN 63 (ANKYRIN 63.1 AND 63.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P516 HUMAN	ANKYRIN 64 (ANKYRIN 64.1 AND 64.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P517 HUMAN	ANKYRIN 65 (ANKYRIN 65.1 AND 65.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P518 HUMAN	ANKYRIN 66 (ANKYRIN 66.1 AND 66.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P519 HUMAN	ANKYRIN 67 (ANKYRIN 67.1 AND 67.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P520 HUMAN	ANKYRIN 68 (ANKYRIN 68.1 AND 68.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P521 HUMAN	ANKYRIN 69 (ANKYRIN 69.1 AND 69.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P522 HUMAN	ANKYRIN 70 (ANKYRIN 70.1 AND 70.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P523 HUMAN	ANKYRIN 71 (ANKYRIN 71.1 AND 71.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P524 HUMAN	ANKYRIN 72 (ANKYRIN 72.1 AND 72.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P525 HUMAN	ANKYRIN 73 (ANKYRIN 73.1 AND 73.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P526 HUMAN	ANKYRIN 74 (ANKYRIN 74.1 AND 74.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P527 HUMAN	ANKYRIN 75 (ANKYRIN 75.1 AND 75.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P528 HUMAN	ANKYRIN 76 (ANKYRIN 76.1 AND 76.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P529 HUMAN	ANKYRIN 77 (ANKYRIN 77.1 AND 77.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P530 HUMAN	ANKYRIN 78 (ANKYRIN 78.1 AND 78.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P531 HUMAN	ANKYRIN 79 (ANKYRIN 79.1 AND 79.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P532 HUMAN	ANKYRIN 80 (ANKYRIN 80.1 AND 80.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P533 HUMAN	ANKYRIN 81 (ANKYRIN 81.1 AND 81.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P534 HUMAN	ANKYRIN 82 (ANKYRIN 82.1 AND 82.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P535 HUMAN	ANKYRIN 83 (ANKYRIN 83.1 AND 83.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P536 HUMAN	ANKYRIN 84 (ANKYRIN 84.1 AND 84.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P537 HUMAN	ANKYRIN 85 (ANKYRIN 85.1 AND 85.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P538 HUMAN	ANKYRIN 86 (ANKYRIN 86.1 AND 86.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P539 HUMAN	ANKYRIN 87 (ANKYRIN 87.1 AND 87.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P540 HUMAN	ANKYRIN 88 (ANKYRIN 88.1 AND 88.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P541 HUMAN	ANKYRIN 89 (ANKYRIN 89.1 AND 89.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P542 HUMAN	ANKYRIN 90 (ANKYRIN 90.1 AND 90.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P543 HUMAN	ANKYRIN 91 (ANKYRIN 91.1 AND 91.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P544 HUMAN	ANKYRIN 92 (ANKYRIN 92.1 AND 92.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P545 HUMAN	ANKYRIN 93 (ANKYRIN 93.1 AND 93.2) (ERYTHROCYTE ANKYRIN)	1544-1571						
P546 HUMAN	ANKYRIN 94 (ANKYRIN 94.1 AND 94.2) (ERYTHROCYTE ANKYRIN)	1544-1571		</				



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CCDS#	PROTEIN	1011164 Medl Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PCAT1	PROTEIN	PCAT1	117-244									
PCAT2	CALRETININ (29 KD CALBINDIN)	PCAT2	12-48									
PCAT3	BETA CASEIN PRECURSOR	PCAT3	427-436									
PCAT4	CATALASE (EC 1.11.1.6)	PCAT4	233-282									
PCAT5	CATHEPSIN D PRECURSOR (EC 3.4.23.5)	PCAT5	41-64									
PCAT6	CATHEPSIN H PRECURSOR (EC 3.4.23.16)	PCAT6	378-395									
PCAT7	CATHEPSIN L PRECURSOR (EC 3.4.23.15) (MAJOR EXCRETED PROTEIN) (NEP)	PCAT7	30-37									
PCAT8	CATHEPSIN S PRECURSOR (EC 3.4.23.31)	PCAT8	118-165									
PCAT9	CAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT B (CBF-B) (NF-Y PROTEIN)	PCAT9	24-38									
PCAT10	CORTICOSTEROID-BINDING GLOBULIN PRECURSOR (CBG) (TRANSCORTIN)	PCAT10	88-122									
PCAT11	CARBOXYPEPTIDASE B PRECURSOR (EC 3.4.17.3) (PANCREAS-SPECIFIC PROTEIN)	PCAT11	69-129									
PCAT12	CARBOXYPEPTIDASE H PRECURSOR (EC 3.4.17.10) (CARBOXYPEPTIDASE E) (CPE)	PCAT12	335-382									
PCAT13	CD31 HOMOLOG (P1-CD31) (FRAGMENT)	PCAT13	33-43									
PCAT14	PROTEIN CD32/HS	PCAT14	209-240									
PCAT15	TRANSCRIPTION INITIATION FACTOR TFIID 300 KD SUBUNIT (TFII-ASSOCIATED)	PCAT15	1298-1342									
PCAT16	MONOCYTE DIFFERENTIATION ANTIGEN CD14 PRECURSOR (MYELOID CELL-SPECIFIC)	PCAT16	143-169									
PCAT17	T-CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T-CELL)	PCAT17	32-63									
PCAT18	T-CELL SURFACE GLYCOPROTEIN CD1E PRECURSOR (CD1E ANTIGEN) (NKG1)	PCAT18	77-104									
PCAT19	B-LYMPHOCYTE ANTIGEN CD20 (B-LYMPHOCYTE SURFACE ANTIGEN B1) (LEU-16)	PCAT19	226-235									
PCAT20	CD20 RECEPTOR PRECURSOR	PCAT20	226-235									
PCAT21	T-CELL SURFACE ANTIGEN CD21 PRECURSOR (T-CELL SURFACE ANTIGEN)	PCAT21	89-119									
PCAT22	HEMOPHETIC PROGENITOR CELL ANTIGEN CD24 PRECURSOR	PCAT22	34-108									
PCAT23	LEUKOCYTE ANTIGEN CD31	PCAT23	101-128									
PCAT24	T-CELL SURFACE GLYCOPROTEIN CD31 GAMMA CHAIN PRECURSOR (T-CELL RECEPTOR)	PCAT24	7-34									
PCAT25	CD31 LIGAND (CD103-L)	PCAT25	96-120									
PCAT26	CD44 ANTIGEN, EPITHELIAL FORM PRECURSOR (CD44E) (PHAGOCYTIC)	PCAT26	318-335									
PCAT27	T-CELL SURFACE GLYCOPROTEIN CD44 PRECURSOR (T-CELL SURFACE ANTIGEN)	PCAT27	44-71									
PCAT28	LEUKOCYTE SURFACE ANTIGEN CD51	PCAT28	87-114									
PCAT29	B-CELL DIFFERENTIATION ANTIGEN CD72 (LY-2)	PCAT29	118-177									
PCAT30	CELL DIVISION PROTEIN KINASE 3 (EC 2.7.1.1)	PCAT30	5-32									
PCAT31	CELL DIVISION PROTEIN KINASE 3 (EC 2.7.1.1) (KINASE P53ALRE)	PCAT31	5-32									
PCAT32	CELL DIVISION PROTEIN KINASE 3 (EC 2.7.1.1) (KINASE P53ALRE)	PCAT32	298-330									
PCAT33	CCAAT-ENHANCER BINDING PROTEIN BETA (CEBP BETA) (NUCLEAR FACTOR)	PCAT33	548-595									
PCAT34	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)	PCAT34	431-466									
PCAT35	CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C)	PCAT35	372-399									
PCAT36	CENTROMERE PROTEIN E (CENP-E) (PROTEIN)	PCAT36	1122-1149									
PCAT37	CERULOPLASMIN PRECURSOR (EC 1.10.3.1) (FERROXIDASE)	PCAT37	1032-1181									
PCAT38	CHOLESTERYL ESTER TRANSFER PROTEIN PRECURSOR	PCAT38	913-940									
PCAT39	CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR (CFTR)	PCAT39	71-108									
PCAT40	COMPACTED CATION CHANNEL PROTEIN (CYCLIC NUCLEOTIDE)	PCAT40	158-189									
PCAT41	CYSTATHIONINE GAMMA-LYASE (EC 4.4.1.1)	PCAT41	216-243									
PCAT42	CHLOROESTERASE-LIKE PROTEIN	PCAT42	315-349									
PCAT43	CHLOROESTERASE-LIKE PROTEIN	PCAT43	17-51									
PCAT44	CHLOROESTERASE-LIKE PROTEIN	PCAT44	56-97									
PCAT45	CHLOROESTERASE-LIKE PROTEIN	PCAT45	210-237									
PCAT46	CHLOROESTERASE-LIKE PROTEIN	PCAT46	431-478									
PCAT47	SODIUM CHANNEL PROTEIN, CARDIAC AND SKELETAL MUSCLE ALPHA-SUBUNIT	PCAT47	112-139									
PCAT48	CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA)	PCAT48	787-814									
PCAT49	CLATHRIN LIGHT CHAIN B (BRAIN AND LYMPHOCYTE LCB)	PCAT49	121-148									
PCAT50	CALCICULIN (PROLACTIN RECEPTOR ASSOCIATED PROTEIN) (PLA) (GROWTH)	PCAT50	123-157									
PCAT51	CLUSTATHIN PRECURSOR (COMPLEMENT-ASSOCIATED PROTEIN SP-40.40)	PCAT51	9-50									
PCAT52	CHROMOGRANIN A PRECURSOR (CGA) (CONTAINS: PANCREASTIN AND WE-14)	PCAT52	36-98									
PCAT53	CELLULAR NEUTROPHILIC FACTOR (CNF)	PCAT53	91-130									
PCAT54	TUMOR-ASSOCIATED ANTIGEN CD47	PCAT54	410-437									
PCAT55	COMPLEMENT C1 PRECURSOR	PCAT55	66-93									
PCAT56	COMPLEMENT C1 PRECURSOR	PCAT56	39-58									
PCAT57	COMPLEMENT C1 PRECURSOR	PCAT57	223-276									
PCAT58	COMPLEMENT C3 PRECURSOR	PCAT58	593-620									
PCAT59	COMPLEMENT C3 PRECURSOR	PCAT59	1292-1319									
PCAT60	COMPLEMENT C3 PRECURSOR	PCAT60	198-242									
PCAT61	COMPLEMENT C3 PRECURSOR	PCAT61	517-544									
PCAT62	COMPLEMENT C3 PRECURSOR	PCAT62	182-198									
PCAT63	COMPLEMENT C1 PRECURSOR	PCAT63	223-261									



PCGENE	101-118, a Moll Search as All Human Protein Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PC001	PROTEIN								
PC002	CYTOCHROME C OXIDASE POLYPEPTIDE 1 (EC 1.9.1.1)	253-280							
PC003	CYTOCHROME P450 VII (CHOLESTEROL 7-ALPHA-MONOXYGENASE)	263-290	246-273						
PC004	CYTOCHROME P450 IIC17 (EC 1.14.14.1) (P450-34C) (FRAGMENT)	109-136							
PC005	CYTOCHROME P450 IIE1 (EC 1.14.14.1) (P450-7) (ETHANOL INDUCIBLE)	231-258							
PC006	CYTOCHROME P450 IIC19 (EC 1.14.14.1) (P450-34C) (FRAGMENT)	112-148	420-447						
PC007	CALAMOTYL-PHOSPHATE SYNTHASE (ANOMIMIA) MITOCHONDRIAL PRECURSOR	410-437							
PC008	MITOCHONDRIAL CARNITINE PALMITOYLTRANSFERASE II PRECURSOR	226-253							
PC009	CYTOCHROME P450 XIAL (P450-X1) (EC 1.14.99.9) (STERIOD 17-ALPHA-1)	234-261							
PC010	CYTOCHROME P450 XIA1 (AROMATASE) (EC 1.14.14.1) (ESTROGEN)	234-261							
PC011	COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR)	94-121	319-270	633-418	724-754	163-790			
PC012	COLONECTAL MUTANT CANCER PROTEIN (MCC PROTEIN)	94-121							
PC013	CAMP RESPONSE ELEMENT BINDING PROTEIN A AND B (CREB-A AND CREB-B)	310-414							
PC014	CAMP RESPONSE ELEMENT BINDING PROTEIN CRE-BP1	60-87	156-177						
PC015	C-REACTIVE PROTEIN PRECURSOR	203-233							
PC016	CLEAVAGE SIGNAL-1 PROTEIN (CS-1)	193-170							
PC017	MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (M-CSF)	6-33							
PC018	CLEAVAGE SIGNALING FACTOR, 10 KD SUBUNIT (CSF1 10 KD SUBUNIT) (CF-1)	6-33							
PC019	ALPHA-CATENIN (CADIHERIN-ASSOCIATED PROTEIN)	608-712							
PC020	ALPHA-CATENIN RELATED PROTEIN (CATENIN ALPHA-2)	608-712							
PC021	GAP JUNCTION BETA-3 PROTEIN (CONNEXIN 36) (CX36)	108-139							
PC022	GAP JUNCTION BETA-2 PROTEIN (CONNEXIN 32) (CX32)	117-144							
PC023	GAP JUNCTION ALPHA-4 PROTEIN (CONNEXIN 37) (CX37)	88-115							
PC024	CYTOCHROME B5	1-42							
PC025	GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN)	89-107	126-153	332-396					
PC026	GUANYLATE CYCLASE SOLUBLE, ALPHA-3 CHAIN (EC 4.6.1.2)	106-133							
PC027	RETINAL GUANYLATE CYCLASE PRECURSOR (EC 4.6.1.2)	824-851							
PC028	CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)	293-270							
PC029	CYTOSTATIN A (CYSTATIN A) (CYSTATIN A)	27-38							
PC030	PROTO-ONCOGENE DBL PRECURSOR (CONTAINS NCF2)	233-283	483-524	766-793	801-843				
PC031	DESMIN	153-180	232-312						
PC032	DESMIN	31-39	112-143	217-244	269-317	382-434	417-467	583-598	630-674
PC033	DESMIN	697-734	718-769	1456-1493	1508-1533				
PC034	ALDENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	31-38							
PC035	ALDENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	86-116	218-265	331-374	353-392	732-759			
PC036	ALDENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	138-165	218-265	331-374	353-392	732-759			
PC037	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	45-76							
PC038	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	110-137							
PC039	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC040	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC041	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC042	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC043	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC044	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC045	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC046	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC047	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC048	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC049	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC050	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC051	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC052	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC053	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC054	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC055	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC056	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC057	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC058	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC059	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC060	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC061	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC062	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC063	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC064	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC065	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC066	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC067	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC068	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC069	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC070	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC071	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC072	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC073	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC074	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC075	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC076	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC077	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC078	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC079	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC080	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC081	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC082	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC083	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC084	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC085	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC086	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC087	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC088	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC089	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC090	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC091	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC092	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC093	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC094	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC095	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC096	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC097	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC098	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC099	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					
PC100	ADENYDE DEHYDROGENASE, DIMERIC NADP-PREFERING (EC 1.3.1.3)	23-74	1009-1037	1100-1127					



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PCGENE	1071194.4 Moll Search for All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PILRB	INTERLEUKIN-1 RECEPTOR, TYPE I PRECURSOR (IL-1R1) (P60)	437-467								
PILRS	INTERLEUKIN-1 RECEPTOR, TYPE II PRECURSOR (IL-1R2)	139-166								
PILRS	INTERLEUKIN-3 RECEPTOR ALPHA CHAIN PRECURSOR (IL-3R-ALPHA)	81-116								
PILRS	INTERLEUKIN-4 PRECURSOR (IL-4) (B-CELL STIMULATORY FACTOR 2) (BSF-2)	112-139								
PILRS	INTERLEUKIN-6 PRECURSOR	94-121								
PILRS	INTERLEUKIN-6 RECEPTOR (IFN-ALPHA-REC)	90-117	100-127	508-535						
PILRS	INTERFERON BETA PRECURSOR (FIBROBLAST)	88-129								
PILRS	INTERFERON-INDUCED 17 KD PROTEIN (CONTAINS INTERFERON-INDUCED 15 KD)	83-121								
PILRS	INSULIN RECEPTOR (P1-54K)	51-78	216-243	393-430						
PILRS	INSULIN RECEPTOR PRECURSOR (EC 2.7.1.112) (IR)	592-619								
PILRS	INVOLOCIN	118-146	218-231	326-353	386-410					
PILRS	10-MYO-INOSITOL-TRISPHOSPHATE 3-KINASE A (EC 2.7.1.127) (INOSITOL)	121-163								
PILRS	PLASMA SERINE PROTEASE (PROTEIN C) INHIBITOR PRECURSOR (PCI)	90-117	206-233							
PILRS	INTERPHOTORECEPTOR RETINOID-BINDING PROTEIN PRECURSOR (IRBP)	670-697								
PILRS	INTERFERON REGULATORY FACTOR 2 (IRF-2)	157-193								
PILRS	91 KD INOSITOL-1,4,5-TRISPHOSPHATE 3-PHOSPHATASE PRECURSOR	215-262								
PILRS	PLATELET MEMBRANE GLYCOPROTEIN IIA PRECURSOR (GPIIa) (COLLAGEN RECEPTOR)	579-608	900-937							
PILRS	FIBRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-5)	230-286	637-695	765-792						
PILRS	INTEGRIN ALPHA-4 PRECURSOR (VLA-4) (INTEGRIN ALPHA-8) (CD49F)	84-911	944-974							
PILRS	LEUKOCYTE ADHESION GLYCOPROTEIN IIA-1 ALPHA CHAIN PRECURSOR (LEUCOC)	356-383								
PILRS	CELL SURFACE GLYCOPROTEIN MAC-1 ALPHA SUBUNIT PRECURSOR (CR-3) ALPHA	1044-1078	110-341	795-822						
PILRS	FIBRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V)	380-384								
PILRS	FIBRONECTIN RECEPTOR BETA SUBUNIT PRECURSOR (INTEGRIN BETA-1) (CD29)	218-245	334-399							
PILRS	CELL SURFACE ADHESION GLYCOPROTEIN IIA-1 CD3 AND P150.95, BETA-	119-166	701-732							
PILRS	PLATELET MEMBRANE GLYCOPROTEIN IIA PRECURSOR (GPIIa) (INTEGRIN BETA-	324-331								
PILRS	INTEGRIN BETA-3 SUBUNIT PRECURSOR (CD109)	343-369								
PILRS	INTEGRIN BETA-3 SUBUNIT PRECURSOR	324-331								
PILRS	INTEGRIN BETA-4 SUBUNIT PRECURSOR	312-318	312-393							
PILRS	INTEGRIN BETA-4 SUBUNIT PRECURSOR	324-331	694-737							
PILRS	INTEGRIN BETA-4 SUBUNIT PRECURSOR	114-161	475-482	772-818						
PILRS	KERATIN, TYPE I CYTOSKELETAL 10 (CYTOKERATIN 10) (K10)	154-187	196-227	337-399	418-462					
PILRS	KERATIN, TYPE I CYTOSKELETAL 11 (CYTOKERATIN 11) (K11)	112-142								
PILRS	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14)	112-143	306-335	393-424						
PILRS	KERATIN, TYPE I CYTOSKELETAL 16 (CYTOKERATIN 16) (K16)	308-339								
PILRS	KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17)	322-352	303-346	393-431						
PILRS	KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18)	87-114	231-296	337-385						
PILRS	KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19)	88-118	317-362	370-397						
PILRS	KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19)	194-228	346-384	390-467						
PILRS	KERATIN, TYPE I CYTOSKELETAL 61 KD	215-248	354-403	461-488						
PILRS	KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (FRAGMENT)	42-72	126-153	189-248						
PILRS	KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (K1)	185-246	332-373							
PILRS	KERATIN, TYPE II CYTOSKELETAL 6 (CYTOKERATIN 6) (K6) (KERATIN)	178-219	325-368	422-449						
PILRS	KERATIN, TYPE II CYTOSKELETAL 8 (CYTOKERATIN 8) (K8)	140-167								
PILRS	KERATIN, TYPE II CYTOSKELETAL 9 (CYTOKERATIN 9) (K9)	7-34	120-161	217-244						
PILRS	6-PHOSPHOGLUTAMATE, MUSCLE TYPE (EC 2.7.1.11) (PHOSPHOGLUTAMATE)	140-167								
PILRS	6-PHOSPHOGLUTAMATE, LIVER TYPE (EC 2.7.1.11) (PHOSPHOGLUTAMATE)	49-40	128-159							
PILRS	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL (EC 2.7.1.112) (P150)	498-525								
PILRS	10 KAPPA CHAIN C REGION	32-45								
PILRS	KALLMAN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE LIKE X-LINK)	310-414								
PILRS	CAMP DEPENDENT PROTEIN KINASE TYPE IALPHA REGULATORY CHAIN	179-206								
PILRS	CAMP DEPENDENT PROTEIN KINASE TYPE IBETA REGULATORY CHAIN	177-204								
PILRS	CAMP DEPENDENT PROTEIN KINASE TYPE IALPHA REGULATORY CHAIN	175-202	390-317							
PILRS	NUCLEAR FACTOR KAPPA-B SUBUNIT-1 (NF-KAPPA-B P105 SUBUNIT)	528-570								
PILRS	CREATINE KINASE, B CHAIN (EC 2.7.1.2)	301-328								
PILRS	TYROSINE PROTEIN KINASE EGF PRECURSOR (EC 2.7.1.112) (EPITHELIAL CELL	466-493								
PILRS	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE PER (EC 2.7.1.112) (P94-FER)	219-246	344-391							



GENE	107176 Motif Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILENAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PFES1 HUMAN	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FES/PS (EC 2.7.1.112) (C-FES)	101-145	291-327					
PFET1 HUMAN	RECEPTOR-RELATED TYROSINE KINASE FLT PRECURSOR (EC 2.7.1.112)	204-235	319-353					
PFH1 HUMAN	MACROPHAGE COLONY STIMULATING FACTOR 1 RECEPTOR PRECURSOR (CSF-1-R)	391-530						
PFY1 HUMAN	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P94-FYN)	199-237						
PCGP1 HUMAN	GTP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (GCK) (EC 2.7.1.37)	17-34						
PFUK1 HUMAN	TYROSINE KINASE MEX RECEPTOR PRECURSOR (EC 2.7.1.112)	648-653						
PFUN1 HUMAN	KUENIN HEAVY CHAIN	135-155	425-453	613-640	689-716	872-899		
PFKIT1 HUMAN	KIT PROTO-ONCOGENE TYROSINE KINASE PRECURSOR (EC 2.7.1.112)	335-263						
PFMET1 HUMAN	HEPATOCYTE GROWTH FACTOR RECEPTOR PRECURSOR (MET PROTO-ONCOGENE)	109-523						
PFNH1 HUMAN	KINNOGEN, HAW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR)	505-532						
PFNS1 HUMAN	GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE PINGTA (EC 2.7.1.1)	81-108						
PFPH1 HUMAN	INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE	148-179	333-312					
PFPI1 HUMAN	MUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.1)	302-469						
PFPL1 HUMAN	PROTEIN KINASE C, BETA TYPE (EC 2.7.1.1) (PKC-BETA) (PKC-L)	318-343						
PFPT1 HUMAN	SEARINE/THREONINE-PROTEIN KINASE PCTAIRE-1 (EC 2.7.1.1)	148-176	209-233					
PFPT1 HUMAN	PRELATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1.40) (CYTOSOLIC THYROID)	243-289						
PFPT1 HUMAN	PRELATE KINASE, M2 ISOZYME (EC 2.7.1.40)	243-289						
PFPT1 HUMAN	PRELATE KINASE, ISOZYME R (EC 2.7.1.40)	243-289						
PFPT1 HUMAN	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE RET (EC 2.7.1.112)	183-217						
PFPS1 HUMAN	EGF PROTO-ONCOGENE TYROSINE KINASE (EC 2.7.1.112) (FRAGMENT)	157-203						
PFSC1 HUMAN	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P40-SRC)	143-170						
PFUT1 HUMAN	LUPUS KU AUTOANTIGEN PROTEIN P78 (70 KD SUBUNIT OF KU ANTIGEN)	335-239						
PFUS1 HUMAN	LUPUS KU AUTOANTIGEN PROTEIN P78 (84 KD SUBUNIT OF KU ANTIGEN)	335-293						
PFV1 HUMAN	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (P41-YES)	309-241						
PFAM1 HUMAN	LAMIN B1	32-66	117-144	152-193	214-241	391-424	480-507	510-539
PFAM1 HUMAN	LAMIN A (70 KD LAMIN)	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN C	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B2	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B3	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B4	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B5	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B6	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B7	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B8	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B9	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B10	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B11	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B12	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B13	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B14	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B15	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B16	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B17	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B18	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B19	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B20	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B21	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B22	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B23	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B24	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B25	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B26	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B27	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B28	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B29	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B30	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B31	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B32	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B33	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B34	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B35	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B36	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B37	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B38	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B39	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B40	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B41	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B42	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B43	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B44	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B45	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B46	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B47	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B48	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B49	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B50	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B51	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B52	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B53	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B54	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B55	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B56	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B57	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B58	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B59	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B60	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B61	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B62	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B63	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B64	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B65	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B66	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B67	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B68	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B69	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B70	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B71	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B72	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B73	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B74	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B75	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B76	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B77	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B78	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B79	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B80	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B81	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B82	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B83	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B84	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B85	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B86	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B87	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B88	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B89	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B90	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B91	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B92	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B93	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B94	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B95	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B96	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B97	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B98	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B99	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B100	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B101	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B102	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B103	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B104	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B105	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B106	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B107	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B108	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B109	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B110	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B111	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B112	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B113	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B114	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B115	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B116	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B117	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B118	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B119	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B120	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B121	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B122	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B123	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B124	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B125	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B126	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B127	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B128	32-66	114-163	292-343				
PFAM1 HUMAN	LAMIN B129	32-66	114-163	292-343				



PCGENE	107178ad Motif Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PMAN1_HUMAN	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.1.1.1) (PHOSPHOMANNANOSE ISOMERASE)	60-87	1147-1182							
PMAN2_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	248-244								
PMAN3_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	414-478								
PMAN4_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	400-449								
PMAN5_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	117-144								
PMAN6_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	235-288								
PMAN7_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	377-407	532-566							
PMAN8_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	31-103	139-173	701-818						
PMAN9_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	91-118	431-438							
PMAN10_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	207-234	319-346	510-537	549-608					
PMAN11_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	18-35	321-348							
PMAN12_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	331-337								
PMAN13_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	331-430								
PMAN14_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	118-144	351-403							
PMAN15_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	326-337								
PMAN16_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	72-99								
PMAN17_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	19-30	2437-2478							
PMAN18_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	378-433	507-548							
PMAN19_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	38-43								
PMAN20_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	187-414	601-628							
PMAN21_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	181-212								
PMAN22_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	448-519								
PMAN23_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	108-150								
PMAN24_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	431-489	610-637							
PMAN25_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	619-646								
PMAN26_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	87-117								
PMAN27_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	283-300	413-461							
PMAN28_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	393-422								
PMAN29_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	119-146								
PMAN30_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	121-148								
PMAN31_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	70-110								
PMAN32_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	42-70								
PMAN33_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	38-75	84-111	132-178	236-324	398-435	440-483			
PMAN34_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	48-75	931-981	997-1044	1088-1122	1192-1234	1266-1332	1360-1408	1442-1479	1418-1532
PMAN35_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	46-73	1640-1681	1683-1710	1801-1838					
PMAN36_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	1707-1734	1827-1838							
PMAN37_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	56-77	95-125	141-188	215-272	403-483	507-552	586-624	685-726	784-818
PMAN38_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	133-160	946-987	1049-1076						
PMAN39_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	133-160	193-280	304-349	423-460	468-526	581-608	641-681	743-798	808-835
PMAN40_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	640-678	846-873							
PMAN41_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	493-519	594-621	705-735						
PMAN42_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	235-282								
PMAN43_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	274-281	310-337							
PMAN44_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	5-32								
PMAN45_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	56-77	82-112	143-195						
PMAN46_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	170-216	644-671							
PMAN47_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	1145-1172	1318-1422	1639-1666						
PMAN48_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	91-128	631-690							
PMAN49_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	97-126	641-681							
PMAN50_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	101-141	164-194	215-230	315-372	372-384	794-826	872-913		
PMAN51_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	318-363								
PMAN52_HUMAN	MACROPHAGE MANNANOSE RECEPTOR PRECURSOR	166-193								



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[illegible]



[illegible]



PGCENE	100% Identity Search on All Human Protein Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
PTAFB HUMAN	TRANSCRIPTION FACTOR JUN-B	196-223								
PTAFD HUMAN	TRANSCRIPTION FACTOR JUN-D	191-223								
PTAUI HUMAN	MICROTUBULE-ASSOCIATED PROTEIN TAU	278-303								
PTAUJ HUMAN	MICROTUBULE-ASSOCIATED PROTEIN TAU, FETAL	211-238								
PTC01 HUMAN	TRANSCOBALANIN I PRECURSOR	201-241								
PTC0J HUMAN	T-COMPLEX PROTEIN I (TCF-1)	310-353								
PTD1 HUMAN	DNA NUCLEOTIDYL TRANSFERASE (EC 2.7.7.1) (TERMINAL ADDITION ENZYME)	315-343								
PTD2 HUMAN	RECEPTOR TYROSINE KINASE TEK PRECURSOR (EC 2.7.1.112) (TKK-6)	61-93								
PTD3 HUMAN	RECEPTOR TYROSINE KINASE TEK PRECURSOR (EC 2.7.1.112) (TKK-6)	64-93								
PTD4 HUMAN	TRANSCRIPTION FACTOR III (TFIIB)	133-162								
PTD5 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD6 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD7 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD8 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD9 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD10 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD11 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD12 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD13 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD14 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD15 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD16 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD17 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD18 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD19 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD20 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD21 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD22 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD23 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD24 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD25 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD26 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD27 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD28 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD29 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD30 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD31 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD32 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD33 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD34 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD35 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD36 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD37 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD38 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD39 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD40 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD41 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD42 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD43 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD44 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD45 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD46 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD47 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD48 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD49 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD50 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD51 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD52 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD53 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD54 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD55 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD56 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD57 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD58 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD59 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD60 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD61 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD62 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD63 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD64 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD65 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD66 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD67 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD68 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD69 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD70 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD71 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD72 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD73 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD74 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD75 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD76 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD77 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD78 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD79 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD80 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD81 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD82 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD83 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD84 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD85 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD86 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD87 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD88 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD89 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD90 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD91 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD92 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD93 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD94 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD95 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD96 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD97 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD98 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD99 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								
PTD100 HUMAN	TRANSCRIPTION FACTOR E (TFE)	133-162								



PCGENE	1071171.4 Model Search for All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
ILK1.HABE	PROTEIN	AREA1											
PXDC.HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM)	264-291											
PXDC.HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-G CELLS (XERODERMA PIGMENTOSUM)	31-110	715-764	1047-1081									
PXDC.HUMAN	DNA-REPAIR PROTEIN XCCCL	71-137											
PXDC.HUMAN	DNA-REPAIR PROTEIN KXCI1 (FRAGMENT)	29-36											
PZM10.HUMAN	ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN KXCI1) (FRAGMENT)	17-62	107-134	1071-1078	1409-1500	2013-2037	2146-2180						
PZM40.HUMAN	ZINC FINGER PROTEIN 40 (HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENTIANCE)	1-20	107-134										
PZM41.HUMAN	ZINC FINGER PROTEIN 41 (ORC1744) (FRAGMENT)	1-20	107-134										
PZM46.HUMAN	ZINC FINGER PROTEIN 46 (ZINC FINGER PROTEIN KUP)	121-149											



**TABLE X**

**Search Results Summary for PCTLZIP,  
P1CTLZIP, and P2CTLZIP Motifs**



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PHEMA MUMPM	133-148									PHEMA IABAN	221-237					PHEMA CVHOC	381-408
PHEMA MUMPR	133-148									PHEMA IABUD	234-250					PHEMA IAAIC	322-338
PHEMA MUMPS	133-148									PHEMA IACKA	234-250					PHEMA IABUD	306-323
PHEMA PIMHW	346-380									PHEMA IACKG	231-247					PHEMA IABUD	320-337
PHEMA PIZH	65-90									PHEMA IACKV	230-246					PHEMA IACKA	320-337
PHEMA PIZHT	65-90									PHEMA IADA1	234-250					PHEMA IACKG	316-333
PHEMA RINDK	306-383									PHEMA IADAJ	237-253					PHEMA IACKP	302-319
PHEMA SVS	7-94									PHEMA IADAZ	234-250					PHEMA IACKP	302-319
PHEMA SV6CM	7-94									PHEMA IADH1	221-237					PHEMA IACKG	319-330
PHEMA SV6CP	7-94									PHEMA IADH2	221-237					PHEMA IACKV	315-332
PHEMA SV8LN	7-94									PHEMA IADH3	221-237					PHEMA IADA1	320-337
PVENV DHV11	42-57									PHEMA IADH4	221-237					PHEMA IADA3	322-339
PVPF7 CAPVK	96-104									PHEMA IADH6	221-237					PHEMA IADG2	320-337
PVSUB VACC8	72-87									PHEMA IADH8	221-237					PHEMA IADH1	306-323
PV001 BP22	242-257									PHEMA IADH7	221-237					PHEMA IADH2	306-323
PV001 HSBVB	169-184									PHEMA IADW2	237-253					PHEMA IADH3	306-323
PV001 HSV11	210-228									PHEMA IADN2	234-250					PHEMA IADH4	306-323
PV006 BPT4	184-198									PHEMA IADN6	221-237					PHEMA IADH6	306-323
PV007 BPT4	666-900									PHEMA IADN7	237-253					PHEMA IADH7	306-323
PV008 HSBV1	134-148									PHEMA IADN8	230-246					PHEMA IADH2	322-338
PV010 BPPH2	183-198									PHEMA IAHAL	230-252					PHEMA IADN2	320-337
PV010 BPPZA	183-198									PHEMA IAHAR	236-251					PHEMA IADU3	322-338
PV010 HSBVA	109-124									PHEMA IAHCB	230-246					PHEMA IADN6	306-323
PV016 BPP1	61-86									PHEMA IAHG7	230-246					PHEMA IADN7	322-339
PV018 BPT4	408-483									PHEMA IAHCO	230-246					PHEMA IADN2	316-332
PV026 BPT4	67-112									PHEMA IAHDS	230-246					PHEMA IADN6	320-337
PV029 HSBV1	20-36									PHEMA IAHFO	236-252					PHEMA IADN2	320-337
PV030 BPPH8	11-84									PHEMA IAHG8	236-252					PHEMA IADN2	319-336
PV036 BPOX2	22-37									PHEMA IAHK7	236-252					PHEMA IADN2	321-338
PV036 HSBVA	108-123									PHEMA IAHLE	230-246					PHEMA IAHCB	316-332
PV037 BPT2	1263-1208									PHEMA IAHLO	230-246					PHEMA IAHG7	316-332
PV037 HSBV1	284-289									PHEMA IAHMI	236-252					PHEMA IAHCD	316-332
PV065 HSBV1	22-37	143-158								PHEMA IAHNM	236-252					PHEMA IAHDE	316-332
PV068 HSBV1	268-283									PHEMA IAHRO	236-252					PHEMA IAHFO	321-338
PV068 HSBV1	102-117									PHEMA IAH8A	236-252					PHEMA IAHK6	321-338
PV068 HSBV1	267-282									PHEMA IAH8P	230-246					PHEMA IAHK7	321-338
PV068 HSBV1	818-933									PHEMA IAH8W	230-246					PHEMA IAHLE	316-332
PV08 BPPH2	234-249									PHEMA IAHTE	236-252					PHEMA IAHLO	316-332
PV08 BPPZA	234-249									PHEMA IAHTO	236-252					PHEMA IAHMI	321-338
PV08 BPPV1R	87-72									PHEMA IAHUR	236-252					PHEMA IAHNM	321-338
PV0F BPPHX	234-249									PHEMA IAKIE	236-251					PHEMA IAHNM	816-932
PV0L3 CVB1	264-278									PHEMA IALEN	236-251					PHEMA IAHPR	316-332
PV0L3 CVB1	264-278									PHEMA IALMAA	236-248					PHEMA IAHRO	321-338
PV0L3 CVB1	264-278									PHEMA IALMAA	236-248					PHEMA IAH8A	316-332
PV0L3 CVB1	264-278									PHEMA IALMAO	237-253					PHEMA IAH8P	316-332
PV0L3 CVBQ	264-278									PHEMA IAHM1	237-253					PHEMA IAH8W	316-332
PV0L3 CVBV	264-278									PHEMA IAHM2	237-253					PHEMA IAHTE	321-338



PVGL2 CVPF3	442-457		PHEMA IAME9	221-237	231-247			PHEMA IANTO	321-336
PVGL2 CVPF8	440-455	504-519	PHEMA IAMIN	85-101				PHEMA IAHUR	321-336
PVGL2 CVPF8	218-233		PHEMA IANT8	237-253				PHEMA IAJAP	317-334
PVGL2 CVPF8	218-233		PHEMA IAU7	221-237				PHEMA IAJAA	316-330
PVGL2 IBV8	1066-1071		PHEMA IARUD	234-250				PHEMA IAJAB	324-341
PVGL2 IBV8	1066-1071		PHEMA IABE2	234-250				PHEMA IAJAO	322-339
PVGL2 IBV8	1066-1071		PHEMA IASH2	234-250				PHEMA IAME1	322-339
PVGL2 IBV8	1066-1071		PHEMA IASTA	230-246				PHEMA IAME2	322-339
PVGL2 IBV8	1066-1071		PHEMA IATAI	235-251				PHEMA IAME6	306-323
PVGL2 IBV8	1066-1071		PHEMA IATKM	234-250				PHEMA IAMIN	316-333
PVGL2 IBV8	1066-1071		PHEMA IATKO	233-248				PHEMA IANT6	322-339
PVGL2 IBV8	1066-1071		PHEMA IATKR	230-246				PHEMA IAPIL	320-337
PVGL2 IBV8	1066-1071		PHEMA IATKW	228-245				PHEMA IAU7	306-323
PVGL2 IBV8	1066-1071		PHEMA IAU83	237-253				PHEMA IARUD	320-337
PVGL2 IBV8	1066-1071		PHEMA IAV17	235-251				PHEMA IABE2	320-337
PVGL2 IBV8	1066-1071		PHEMA IAXIA	235-251				PHEMA IABH2	321-338
PVGL2 IBV8	1066-1071		PHEMA IAZCO	237-253				PHEMA IABTA	316-332
PVGL2 IBV8	1066-1071		PHEMA IAZH2	221-237				PHEMA IATKM	320-337
PVGL2 IBV8	1066-1071		PHEMA IAZH3	221-237				PHEMA IAU7	323-340
PVGL2 IBV8	1066-1071		PHEMA IAZUK	237-253				PHEMA IAZCO	322-339
PVGL2 IBV8	1066-1071		PHEMA IABAA	116-131	266-310			PHEMA IAZH2	306-323
PVGL2 IBV8	1066-1071		PHEMA INB8E	123-139	303-318			PHEMA IAZH3	306-323
PVGL2 IBV8	1066-1071		PHEMA INB8O	116-132	293-308			PHEMA IAZUK	322-339
PVGL2 IBV8	1066-1071		PHEMA INB8N	123-139	301-316			PHEMA MUMPM	101-116
PVGL2 IBV8	1066-1071		PHEMA INB8U	105-124	286-301			PHEMA MUMPR	101-116
PVGL2 IBV8	1066-1071		PHEMA INB8U	119-135	286-311			PHEMA MUMPS	101-116
PVGL2 IBV8	1066-1071		PHEMA INB8L	116-132	293-308			PHEMA NDVA	93-110
PVGL2 IBV8	1066-1071		PHEMA INB8K	106-124	268-303			PHEMA NDVB	93-110
PVGL2 IBV8	1066-1071		PHEMA INB8B	120-136	298-314			PHEMA NDVD	93-110
PVGL2 IBV8	1066-1071		PHEMA INB8D	123-139	302-317			PHEMA NDVH	93-110
PVGL2 IBV8	1066-1071		PHEMA INB8E	113-129	292-307			PHEMA NDVI	93-110
PVGL2 IBV8	1066-1071		PHEMA INB8M	116-132	296-311			PHEMA NDVM	93-110
PVGL2 IBV8	1066-1071		PHEMA INB8E	105-124	288-303			PHEMA NDVO	93-110
PVGL2 IBV8	1066-1071		PHEMA INB8A	123-139	301-316			PHEMA NDVT0	93-110
PVGL2 IBV8	1066-1071		PHEMA INB8R	123-139	301-316			PHEMA NDVU	93-110
PVGL2 IBV8	1066-1071		PHEMA INB8I	119-135	298-313			PHEMA PHODV	306-63
PVGL2 IBV8	1066-1071		PHEMA INB8J	116-132	294-309			PHEMA PIHW	486-503
PVGL2 IBV8	1066-1071		PHEMA INB8S	116-132	296-311			PHEMA PI3B	111-126
PVGL2 IBV8	1066-1071		PHEMA INB8V	116-132	298-311			PHEMA PI3H4	111-126
PVGL2 IBV8	1066-1071		PHEMA INB8K	123-139	303-318			PHEMA PI3HA	111-126
PVGL2 IBV8	1066-1071		PHEMA INB8B	108-124	286-301			PHEMA PI3HT	111-126
PVGL2 IBV8	1066-1071		PHEMA MUMPM	133-148				PHEMA PI3HU	111-126
PVGL2 IBV8	1066-1071		PHEMA MUMPR	133-148				PHEMA PI3HV	111-126
PVGL2 IBV8	1066-1071		PHEMA MUMPS	133-148				PHEMA PI3HW	111-126
PVGL2 IBV8	1066-1071		PHEMA PI1HW	345-360				PHEMA PI3HX	111-126
PVGL2 IBV8	1066-1071		PHEMA PI2H	65-81				PHEMA PI4HA	50-67
PVGL2 IBV8	1066-1071		PHEMA PI2HT	65-81					



PVMT2 IALE1	26-40	PIEMA P13B	324-340				PIEMA 8V41	86-102	
PVMT2 IALE2	26-40	PIEMA P13H4	324-340				PIEMA 8V6	84-101	
PVMT2 IAMAN	26-40	PIEMA P13HA	324-340				PIEMA 8V6CM	84-101	
PVMT2 IAPUE	26-40	PIEMA P13HT	324-340				PIEMA 8V6CP	84-101	
PVMT2 IASIN	26-40	PIEMA P13HU	324-340				PIEMA 8V6LN	84-101	
PVMT2 IAUDD	26-40	PIEMA P13HV	324-340				PVFB5 VACCC	280-287	
PVMT2 IAWIL	26-40	PIEMA P13HW	324-340				PVFB5 VACCP	280-287	
PVMT9 MTXVL	226-241	PIEMA P13HX	324-340				PVFB5 VACCV	281-288	
		PIEMA RINDK	306-383				PVFB5 VACCC	176-183	
		PIEMA 8V6	7-84				PVFB5 VACCV	176-183	
		PIEMA 8V6CM	7-84				PVQ27 H8V8A	209-220	
		PIEMA 8V6CP	7-84				PVQ28 H8V11	173-180	
		PIEMA 8V6LN	7-84				PVQ39 H8V11	648-668	
		PVENV DRV11	42-67				PVQ43 H8V11	108-128	521-538
		PVENV EAV	28-41				PVQ67 H8V11	171-188	
		PVFT2 FOMPV	88-104				PVQ72 H8V11	1262-1268	
		PVFT7 CAPVK	89-104				PVQF1 8V6	3073-3090	
		PVFB5 VACCB	72-87				PVQL2 8V6	1094-1111	
		PVQ01 H8VEB	188-184				PVQLB H8VE1	738-763	
		PVQ01 H8V11	208-226				PVQLB H8VE4	676-682	
		PVQ08 H8V11	134-148			317-332	PVQLB H8VEA	738-763	
		PVQ10 H8V8A	108-124				PVQLB H8VEB	738-763	
		PVQ11 H8V11	103-118				PVQLB H8VEL	738-763	
		PVQ22 H8V11	270-280				PVQLB ILTV8	587-614	
		PVQ1 8PV1R	76-92				PVQLB ILTV8	607-624	
		PVQ28 H8V11	20-35				PVQLB ILTVT	607-624	
		PVQ88 BPOX2	22-37				PVQLC PRVIF	180-187	
		PVQ36 H8V8A	108-123				PVQLF 8V6	401-418	
		PVQ37 H8V11	204-280				PVQLH H8V11	385-382	
		PVQ41 H8V11	244-260				PVQLH H8V1E	248-262	803-820
		PVQ46 H8V11	1244-1260				PVQLH H8V1E	248-262	803-820
		PVQ55 H8V11	22-37			143-168	PVQLH H8V11	43-60	
		PVQ56 H8V11	205-283				PVQLM BUNL7	61-86	
		PVQ58 H8V11	101-117				PVQLM BUNH	81-88	
		PVQ66 H8V8A	130-146			330-346	PVQLM PUUMH	712-720	
		PVQ68 H8V11	207-282				PVQLM PUUMH	712-720	
		PVQ71 H8V8A	88-106				PVQLM RVFV	344-361	
		PVQ8 BPH2	234-249				PVQLM RVFVZ	344-361	
		PVQ8 BPTA	234-249				PVQLY LA980	12-84	
		PVQ8 8PV1R	67-72				PVQLY LA88J	12-84	
		PVQ81 8V8	2210-2228				PVQLY LYCVA	12-84	
		PVQL2 CV8F	123-138			174-190	PVQLY LYCVW	12-84	
		PVQL2 CV8L9	123-138			174-190	PVQLY MOPEI	12-84	
		PVQL2 CV8LY	123-138			174-190	PVQLY REOVD	280-287	
		PVQL2 CV8M	123-138			174-190	PVQLY REOVL	280-287	
		PVQL2 CV8Q	31-47			123-138			



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PVMT2 IAFPR	28-40
PVMT2 IAFPW	28-40
PVMT2 IALET	28-40
PVMT2 IALEZ	28-40
PVMT2 IAMAN	28-40
PVMT2 IAPUE	28-40
PVMT2 IABIN	28-40
PVMT2 IAUDD	28-40
PVMT2 IAWIL	28-40
PVMT9 MYXVL	270-241



## TABLE XI

Search Results Summary for P3CTLZIP, P4CTLZIP,  
P5CTLZIP, and P6CTLZIP Motifs



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PVMO1 VACCV	183-101	126-144	PVQL3 CVM4	889-1018		PVENY THOOV	366-378		PHEMA P12H	13-34	
PVM1 REOVD	227-246		PVQL2 CVM4S	847-889		PVQ01 VACCC	288-318		PHEMA P12H	13-34	
PVM1 REOVL	227-246		PVQL3 CVMJH	868-877		PVQ01 VACCV	289-257		PHEMA BV8	7-28	378-400
PVMAT HREVA	44-82		PVQL3 CVPF8	84-83	1030-1062	PVQ01 VARV	289-318		PHEMA BV6CM	7-28	378-400
PVMAT NDVA	180-208		PVQL3 CVPFU	84-83	1030-1055	PVQ08 VACCC	31-51		PHEMA BV6CP	7-28	378-400
PVMAT NDVB	180-208		PVQL3 CVPFB	814-833		PVQ08 VARV	31-51		PHEMA BV6LN	7-28	378-400
PVMP CAMVC	183-201		PVQL3 CVPFM	814-833		PVQ08 BPFF1	26-46		PVQ01 HSEB	189-180	
PVMP CAMVD	183-201		PVQL3 FIPV	1041-1060		PVQ12 HSNV1	151-171		PVQ01 HSNV1	689-610	
PVMP CAMVE	183-201		PVQL3 IBV8	588-607	771-780	PVQ22 HSNV1	300-320		PVQ23 HSNV1	314-335	
PVMP CAMVN	183-201		PVQL3 IBV8	587-606	770-789	PVQ38 HSNV1	640-668	970-990	PVQ37 BPOX2	65-86	
PVMP CAMVS	183-201		PVQL3 IBVD2	588-607	771-789	PVQ61 HSNV1	29-48		PVQ43 HSNV1	167-178	
PVMP CAMVW	183-201		PVQL3 IBVK	587-606	770-789	PVQ63 HSNV1	338-356		PVQ56 HSNV1	288-309	
PVMP FMVD	180-188		PVQL2 BVM	587-606	770-780	PVQ66 HSNV1	117-137		PVQ56 HSNV1	85-108	
			PVQL8 HCMVA	708-726		PVQ74 HSNV1	124-144		PVQ59 HSNV1	1155-1178	
			PVQL8 HCMVT	707-726		PVQL2 IBV8	328-348		PVQ59 HSNV1	208-287	
			PVQL8 HSNV8U	117-138		PVQL2 IBV8	327-347		PVQ80 HSNV1	30-51	
			PVQL8 ILTV8	258-276		PVQL2 IBVD2	328-348		PVQ83 HSNV1	238-258	
			PVQL8 ILTVS	268-285		PVQL2 IBVD3	328-348		PVQF1 IBV8	1650-1877	
			PVQL8 ILTVT	268-285		PVQL2 IBVK	327-347		PVQH3 HCMVA	167-178	
			PVQL8 HSNV11	3-84	487-488	PVQL2 IBVM	327-347	378-388	PVQL2 CVBF	1259-1280	
			PVQL8 HSNV1K	3-84	487-488	PVQL2 IBVU2	310-330		PVQL2 CVBL8	1259-1280	
			PVQL8 HSNVBC	476-484		PVQL8 EBV	732-752		PVQL2 CVBL8	1259-1280	
			PVQL8 CHAV	438-456		PVQL8 HCMVA	750-770		PVQL2 CVBM	1259-1280	
			PVQL8 RABVH	372-391		PVQL8 HCMVT	751-771		PVQL2 CVBQ	1259-1280	
			PVQL8 HSNV8	44-83		PVQL8 HSNV29	78-88		PVQL2 CVBV	1259-1280	
			PVQL1 VZVD	378-267		PVQL8 HSNV2H	78-88		PVQL2 CVM4	1312-1338	
			PVQLM BUNOE	117-138		PVQL8 HSNV29	65-86		PVQL2 CVM4S	1286-1288	
			PVQLM PHV	162-171		PVQL8 HSNV8U	72-92		PVQL2 CVMJH	1176-1197	
			PVQLM PTPV	887-1018		PVQL8 HSNV82	279-299		PVQL8 HSNV11	83-104	
			PVQLM PUUMH	166-174		PVQL8 HSNV8A	63-83		PVQL8 HSNV1F	82-103	
			PVQLM PUUMS	166-174		PVQL8 MCMV8	738-758		PVQL8 HSNV1K	82-103	
			PVQLM RVFV	830-849		PVQLF P13H4	283-303		PVQL8 HSNV1P	83-104	
			PVQLM RVFV2	830-849		PVQL8 RABVE	454-474		PVQL8 MCMV8	135-150	
			PVQLM UUK	666-674		PVQL8 RABVH	454-474		PVQLC PVFV	448-467	
			PVQLY LYCVW	88-108		PVQL8 RABVP	454-474		PVQLF CDVO	338-357	
			PVQLB CPMV	1185-1104		PVQL8 RABV8	454-474		PVQLF MEABE	224-246	
			PVQLB REOVD	521-540		PVQL8 RABVT	454-474		PVQLF MEAB1	227-248	
			PVQLB CVBM	171-180		PVQLH MCMV8	670-680		PVQLF MEABY	224-246	
			PVQLB CVH22	136-156		PVQLM BUNL7	1325-1346		PVQLF MUMPM	448-467	
			PVQLB CVF8	174-183		PVQLM BUN8H	1325-1346		PVQLF MUMPR	448-467	
			PVQLB CVPFU	174-183		PVQLM BUNYV	988-1018		PVQLF MUMPS	448-467	
			PVQLB CVPFM	174-183		PVQLM HANTB	988-1018		PVQLF PHODV	306-328	
			PVQLB CVTK8	171-180		PVQLM HANTH	1000-1020		PVQLF PIHIC	460-471	
						PVQLM HANTL	1001-1021		PVQLF PI2H	460-471	
						PVQLM HANTY	1001-1021		PVQLF PI2HG	460-471	
						PVQLM RVFV2	1156-1178		PVQLF PI2HT	460-471	
						PVQLM SEOUR	1000-1020		PVQLF PI3B	406-428	483-474



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PVM9A HPBVZ	23-264
PVMT2 IAHNN	26-40
PVMT2 IABAN	26-40
PVMT2 IAFOW	26-40
PVMT2 IAFPR	26-40
PVMT2 IAFPW	26-40
PVMT2 IALE1	26-40
PVMT2 IALE2	26-40
PVMT2 IAMAN	26-40
PVMT2 IAPUE	26-40
PVMT2 IABIN	26-40
PVMT2 IAUDO	26-40
PVMT2 IAWIL	26-40



## TABLE XII

Search Results Summary for P7CTLZIP,  
P8CTLZIP, and P9CTLZIP Motifs



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## TABLE XIII

### SEARCH RESULTS SUMMARY FOR P12LZIPC MOTIF



GENE	FUNCTION	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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ECCESE	FUNCTION	ALL VIRUSES (No. Distributions)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 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451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 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784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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CCODE	PROTEIN	PIK12121P	AB Virus (No Restriction)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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264



PCGENE	PICTEST2P	AB Virus (No Entry) (g)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
ELK MARIE	PROTEIN	HUMAN FOAMY VIRUS (TYPE 1)	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-204	182-2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FIGURE	PROJECT	ALL VIRUSES (No. Bacteriophages)	ORCA 1	ORCA 2	ORCA 3	ORCA 4	ORCA 5	ORCA 6	ORCA 7	ORCA 8	ORCA 9	ORCA 10	ORCA 11	ORCA 12	ORCA 13	ORCA 14	ORCA 15	ORCA 16	ORCA 17	ORCA 18	ORCA 19	ORCA 20	ORCA 21	ORCA 22	ORCA 23	ORCA 24	ORCA 25	ORCA 26	ORCA 27	ORCA 28	ORCA 29	ORCA 30	ORCA 31	ORCA 32	ORCA 33	ORCA 34	ORCA 35	ORCA 36	ORCA 37	ORCA 38	ORCA 39	ORCA 40	ORCA 41	ORCA 42	ORCA 43	ORCA 44	ORCA 45	ORCA 46	ORCA 47	ORCA 48	ORCA 49	ORCA 50	ORCA 51	ORCA 52	ORCA 53	ORCA 54	ORCA 55	ORCA 56	ORCA 57	ORCA 58	ORCA 59	ORCA 60	ORCA 61	ORCA 62	ORCA 63	ORCA 64	ORCA 65	ORCA 66	ORCA 67	ORCA 68	ORCA 69	ORCA 70	ORCA 71	ORCA 72	ORCA 73	ORCA 74	ORCA 75	ORCA 76	ORCA 77	ORCA 78	ORCA 79	ORCA 80	ORCA 81	ORCA 82	ORCA 83	ORCA 84	ORCA 85	ORCA 86	ORCA 87	ORCA 88	ORCA 89	ORCA 90	ORCA 91	ORCA 92	ORCA 93	ORCA 94	ORCA 95	ORCA 96	ORCA 97	ORCA 98	ORCA 99	ORCA 100	ORCA 101	ORCA 102	ORCA 103	ORCA 104	ORCA 105	ORCA 106	ORCA 107	ORCA 108	ORCA 109	ORCA 110	ORCA 111	ORCA 112	ORCA 113	ORCA 114	ORCA 115	ORCA 116	ORCA 117	ORCA 118	ORCA 119	ORCA 120	ORCA 121	ORCA 122	ORCA 123	ORCA 124	ORCA 125	ORCA 126	ORCA 127	ORCA 128	ORCA 129	ORCA 130	ORCA 131	ORCA 132	ORCA 133	ORCA 134	ORCA 135	ORCA 136	ORCA 137	ORCA 138	ORCA 139	ORCA 140	ORCA 141	ORCA 142	ORCA 143	ORCA 144	ORCA 145	ORCA 146	ORCA 147	ORCA 148	ORCA 149	ORCA 150	ORCA 151	ORCA 152	ORCA 153	ORCA 154	ORCA 155	ORCA 156	ORCA 157	ORCA 158	ORCA 159	ORCA 160	ORCA 161	ORCA 162	ORCA 163	ORCA 164	ORCA 165	ORCA 166	ORCA 167	ORCA 168	ORCA 169	ORCA 170	ORCA 171	ORCA 172	ORCA 173	ORCA 174	ORCA 175	ORCA 176	ORCA 177	ORCA 178	ORCA 179	ORCA 180	ORCA 181	ORCA 182	ORCA 183	ORCA 184	ORCA 185	ORCA 186	ORCA 187	ORCA 188	ORCA 189	ORCA 190	ORCA 191	ORCA 192	ORCA 193	ORCA 194	ORCA 195	ORCA 196	ORCA 197	ORCA 198	ORCA 199	ORCA 200	ORCA 201	ORCA 202	ORCA 203	ORCA 204	ORCA 205	ORCA 206	ORCA 207	ORCA 208	ORCA 209	ORCA 210	ORCA 211	ORCA 212	ORCA 213	ORCA 214	ORCA 215	ORCA 216	ORCA 217	ORCA 218	ORCA 219	ORCA 220	ORCA 221	ORCA 222	ORCA 223	ORCA 224	ORCA 225	ORCA 226	ORCA 227	ORCA 228	ORCA 229	ORCA 230	ORCA 231	ORCA 232	ORCA 233	ORCA 234	ORCA 235	ORCA 236	ORCA 237	ORCA 238	ORCA 239	ORCA 240	ORCA 241	ORCA 242	ORCA 243	ORCA 244	ORCA 245	ORCA 246	ORCA 247	ORCA 248	ORCA 249	ORCA 250	ORCA 251	ORCA 252	ORCA 253	ORCA 254	ORCA 255	ORCA 256	ORCA 257	ORCA 258	ORCA 259	ORCA 260	ORCA 261	ORCA 262	ORCA 263	ORCA 264	ORCA 265	ORCA 266	ORCA 267	ORCA 268	ORCA 269	ORCA 270	ORCA 271	ORCA 272	ORCA 273	ORCA 274	ORCA 275	ORCA 276	ORCA 277	ORCA 278	ORCA 279	ORCA 280	ORCA 281	ORCA 282	ORCA 283	ORCA 284	ORCA 285	ORCA 286	ORCA 287	ORCA 288	ORCA 289	ORCA 290	ORCA 291	ORCA 292	ORCA 293	ORCA 294	ORCA 295	ORCA 296	ORCA 297	ORCA 298	ORCA 299	ORCA 300	ORCA 301	ORCA 302	ORCA 303	ORCA 304	ORCA 305	ORCA 306	ORCA 307	ORCA 308	ORCA 309	ORCA 310	ORCA 311	ORCA 312	ORCA 313	ORCA 314	ORCA 315	ORCA 316	ORCA 317	ORCA 318	ORCA 319	ORCA 320	ORCA 321	ORCA 322	ORCA 323	ORCA 324	ORCA 325	ORCA 326	ORCA 327	ORCA 328	ORCA 329	ORCA 330	ORCA 331	ORCA 332	ORCA 333	ORCA 334	ORCA 335	ORCA 336	ORCA 337	ORCA 338	ORCA 339	ORCA 340	ORCA 341	ORCA 342	ORCA 343	ORCA 344	ORCA 345	ORCA 346	ORCA 347	ORCA 348	ORCA 349	ORCA 350	ORCA 351	ORCA 352	ORCA 353	ORCA 354	ORCA 355	ORCA 356	ORCA 357	ORCA 358	ORCA 359	ORCA 360	ORCA 361	ORCA 362	ORCA 363	ORCA 364	ORCA 365	ORCA 366	ORCA 367	ORCA 368	ORCA 369	ORCA 370	ORCA 371	ORCA 372	ORCA 373	ORCA 374	ORCA 375	ORCA 376	ORCA 377	ORCA 378	ORCA 379	ORCA 380	ORCA 381	ORCA 382	ORCA 383	ORCA 384	ORCA 385	ORCA 386	ORCA 387	ORCA 388	ORCA 389	ORCA 390	ORCA 391	ORCA 392	ORCA 393	ORCA 394	ORCA 395	ORCA 396	ORCA 397	ORCA 398	ORCA 399	ORCA 400	ORCA 401	ORCA 402	ORCA 403	ORCA 404	ORCA 405	ORCA 406	ORCA 407	ORCA 408	ORCA 409	ORCA 410	ORCA 411	ORCA 412	ORCA 413	ORCA 414	ORCA 415	ORCA 416	ORCA 417	ORCA 418	ORCA 419	ORCA 420	ORCA 421	ORCA 422	ORCA 423	ORCA 424	ORCA 425	ORCA 426	ORCA 427	ORCA 428	ORCA 429	ORCA 430	ORCA 431	ORCA 432	ORCA 433	ORCA 434	ORCA 435	ORCA 436	ORCA 437	ORCA 438	ORCA 439	ORCA 440	ORCA 441	ORCA 442	ORCA 443	ORCA 444	ORCA 445	ORCA 446	ORCA 447	ORCA 448	ORCA 449	ORCA 450	ORCA 451	ORCA 452	ORCA 453	ORCA 454	ORCA 455	ORCA 456	ORCA 457	ORCA 458	ORCA 459	ORCA 460	ORCA 461	ORCA 462	ORCA 463	ORCA 464	ORCA 465	ORCA 466	ORCA 467	ORCA 468	ORCA 469	ORCA 470	ORCA 471	ORCA 472	ORCA 473	ORCA 474	ORCA 475	ORCA 476	ORCA 477	ORCA 478	ORCA 479	ORCA 480	ORCA 481	ORCA 482	ORCA 483	ORCA 484	ORCA 485	ORCA 486	ORCA 487	ORCA 488	ORCA 489	ORCA 490	ORCA 491	ORCA 492	ORCA 493	ORCA 494	ORCA 495	ORCA 496	ORCA 497	ORCA 498	ORCA 499	ORCA 500	ORCA 501	ORCA 502	ORCA 503	ORCA 504	ORCA 505	ORCA 506	ORCA 507	ORCA 508	ORCA 509	ORCA 510	ORCA 511	ORCA 512	ORCA 513	ORCA 514	ORCA 515	ORCA 516	ORCA 517	ORCA 518	ORCA 519	ORCA 520	ORCA 521	ORCA 522	ORCA 523	ORCA 524	ORCA 525	ORCA 526	ORCA 527	ORCA 528	ORCA 529	ORCA 530	ORCA 531	ORCA 532	ORCA 533	ORCA 534	ORCA 535	ORCA 536	ORCA 537	ORCA 538	ORCA 539	ORCA 540	ORCA 541	ORCA 542	ORCA 543	ORCA 544	ORCA 545	ORCA 546	ORCA 547	ORCA 548	ORCA 549	ORCA 550	ORCA 551	ORCA 552	ORCA 553	ORCA 554	ORCA 555	ORCA 556	ORCA 557	ORCA 558	ORCA 559	ORCA 560	ORCA 561	ORCA 562	ORCA 563	ORCA 564	ORCA 565	ORCA 566	ORCA 567	ORCA 568	ORCA 569	ORCA 570	ORCA 571	ORCA 572	ORCA 573	ORCA 574	ORCA 575	ORCA 576	ORCA 577	ORCA 578	ORCA 579	ORCA 580	ORCA 581	ORCA 582	ORCA 583	ORCA 584	ORCA 585	ORCA 586	ORCA 587	ORCA 588	ORCA 589	ORCA 590	ORCA 591	ORCA 592	ORCA 593	ORCA 594	ORCA 595	ORCA 596	ORCA 597	ORCA 598	ORCA 599	ORCA 600	ORCA 601	ORCA 602	ORCA 603	ORCA 604	ORCA 605	ORCA 606	ORCA 607	ORCA 608	ORCA 609	ORCA 610	ORCA 611	ORCA 612	ORCA 613	ORCA 614	ORCA 615	ORCA 616	ORCA 617	ORCA 618	ORCA 619	ORCA 620	ORCA 621	ORCA 622	ORCA 623	ORCA 624	ORCA 625	ORCA 626	ORCA 627	ORCA 628	ORCA 629	ORCA 630	ORCA 631	ORCA 632	ORCA 633	ORCA 634	ORCA 635	ORCA 636	ORCA 637	ORCA 638	ORCA 639	ORCA 640	ORCA 641	ORCA 642	ORCA 643	ORCA 644	ORCA 645	ORCA 646	ORCA 647	ORCA 648	ORCA 649	ORCA 650	ORCA 651	ORCA 652	ORCA 653	ORCA 654	ORCA 655	ORCA 656	ORCA 657	ORCA 658	ORCA 659	ORCA 660	ORCA 661	ORCA 662	ORCA 663	ORCA 664	ORCA 665	ORCA 666	ORCA 667	ORCA 668	ORCA 669	ORCA 670	ORCA 671	ORCA 672	ORCA 673	ORCA 674	ORCA 675	ORCA 676	ORCA 677	ORCA 678	ORCA 679	ORCA 680	ORCA 681	ORCA 682	ORCA 683	ORCA 684	ORCA 685	ORCA 686	ORCA 687	ORCA 688	ORCA 689	ORCA 690	ORCA 691	ORCA 692	ORCA 693	ORCA 694	ORCA 695	ORCA 696	ORCA 697	ORCA 698	ORCA 699	ORCA 700	ORCA 701	ORCA 702	ORCA 703	ORCA 704	ORCA 705	ORCA 706	ORCA 707	ORCA 708	ORCA 709	ORCA 710	ORCA 711	ORCA 712	ORCA 713	ORCA 714	ORCA 715	ORCA 716	ORCA 717	ORCA 718	ORCA 719	ORCA 720	ORCA 721	ORCA 722	ORCA 723	ORCA 724	ORCA 725	ORCA 726	ORCA 727	ORCA 728	ORCA 729	ORCA 730	ORCA 731	ORCA 732	ORCA 733	ORCA 734	ORCA 735	ORCA 736	ORCA 737	ORCA 738	ORCA 739	ORCA 740	ORCA 741	ORCA 742	ORCA 743	ORCA 744	ORCA 745	ORCA 746	ORCA 747	ORCA 748	ORCA 749	ORCA 750	ORCA 751	ORCA 752	ORCA 753	ORCA 754	ORCA 755	ORCA 756	ORCA 757	ORCA 758	ORCA 759	ORCA 760	ORCA 761	ORCA 762	ORCA 763	ORCA 764	ORCA 765	ORCA 766	ORCA 767	ORCA 768	ORCA 769	ORCA 770	ORCA 771	ORCA 772	ORCA 773	ORCA 774	ORCA 775	ORCA 776	ORCA 777	ORCA 778	ORCA 779	ORCA 780	ORCA 781	ORCA 782	ORCA 783	ORCA 784	ORCA 785	ORCA 786	ORCA 787	ORCA 788	ORCA 789	ORCA 790	ORCA 791	ORCA 792	ORCA 793	ORCA 794	ORCA 795	ORCA 796	ORCA 797	ORCA 798	ORCA 799	ORCA 800	ORCA 801	ORCA 802	ORCA 803	ORCA 804	ORCA 805	ORCA 806	ORCA 807	ORCA 808	ORCA 809	ORCA 810	ORCA 811	ORCA 812	ORCA 813	ORCA 814	ORCA 815	ORCA 816	ORCA 817	ORCA 818	ORCA 819	ORCA 820	ORCA 821	ORCA 822	ORCA 823	ORCA 824	ORCA 825	ORCA 826	ORCA 827	ORCA 828	ORCA 829	ORCA 830	ORCA 831	ORCA 832	ORCA 833	ORCA 834	ORCA 835	ORCA 836	ORCA 837	ORCA 838	ORCA 839	ORCA 840	ORCA 841	ORCA 842	ORCA 843	ORCA 844	ORCA 845	ORCA 846	ORCA 847	ORCA 848	ORCA 849	ORCA 850	ORCA 851	ORCA 852	ORCA 853	ORCA 854	ORCA 855	ORCA 856	ORCA 857	ORCA 858	ORCA 859	ORCA 860	ORCA 861	ORCA 862	ORCA 863	ORCA 864	ORCA 865	ORCA 866	ORCA 867	ORCA 868	ORCA 869	ORCA 870	ORCA 871	ORCA 872	ORCA 873	ORCA 874	ORCA 875	ORCA 876	ORCA 877	ORCA 878	ORCA 879	ORCA 880	ORCA 881	ORCA 882	ORCA 883	ORCA 884	ORCA 885	ORCA 886	ORCA 887	ORCA 888	ORCA 889	ORCA 890	ORCA 891	ORCA 892	ORCA 893	ORCA 894	ORCA 895	ORCA 896	ORCA 897	ORCA 898	ORCA 899	ORCA 900	ORCA 901	ORCA 902	ORCA 903	ORCA 904	ORCA 905	ORCA 906	ORCA 907	ORCA 908	ORCA 909	ORCA 910	ORCA 911	ORCA 912	ORCA 913	ORCA 914	ORCA 915	ORCA 916	ORCA 917	ORCA 918	ORCA 919	ORCA 920	ORCA 921	ORCA 922	ORCA 923	ORCA 924	ORCA 925	ORCA 926	ORCA 927	ORCA 928	ORCA 929	ORCA 930	ORCA 931	ORCA 932	ORCA 933	ORCA 934	ORCA 935	ORCA 936	ORCA 937	ORCA 938	ORCA 939	ORCA 940	ORCA 941	ORCA 942	ORCA 943	ORCA 944	ORCA 945	ORCA 946	ORCA 947	ORCA 948	ORCA 949	ORCA 950	ORCA 951	ORCA 952	ORCA 953	ORCA 954	ORCA 955	ORCA 956	ORCA 957	ORCA 958	ORCA 959	ORCA 960	ORCA 961	ORCA 962	ORCA 963	ORCA 964	ORCA 965	ORCA 966	ORCA 967	ORCA 968	ORCA 969	ORCA 970	ORCA 971	ORCA 972	ORCA 973	ORCA 974	ORCA 975	ORCA 976	ORCA 977	ORCA 978	ORCA 979	ORCA 980	ORCA 981	ORCA 982	ORCA 983	ORCA 984	ORCA 985	ORCA 986	ORCA 987	ORCA 988	ORCA 989	ORCA 990	ORCA 991	ORCA 992	ORCA 993	ORCA 994	ORCA 995	ORCA 996	ORCA 997	ORCA 998	ORCA 999	ORCA 1000
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268



PCGCODE	FILE NAME	PLICTLZIP	AB Virus (No. Bacteriophage 902)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PCG001	PC																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													



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GENE	FUNCTION	ALL Viruses (No. Bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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272



GENE	PII CT/PII	AB Virus (No Restriction)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILE NAME	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
P1001 HCV	HYPOTHETICAL PROTEIN UL113	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-21						AREA7
P1002 HCV	URACIL-DNA GLYCOSYLASE	TOWNSHIP VIRUS (STRAIN PP-1)	12-31						
P1003 HCV	URACIL-DNA GLYCOSYLASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD169)	12-31						
P1004 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	12-103						
P1005 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1006 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1007 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1008 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1009 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1010 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1011 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1012 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1013 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1014 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1015 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1016 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1017 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1018 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1019 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1020 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1021 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1022 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1023 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1024 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1025 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1026 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1027 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1028 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1029 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1030 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1031 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1032 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1033 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1034 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1035 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1036 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1037 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1038 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1039 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1040 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1041 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1042 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1043 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1044 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1045 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1046 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1047 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1048 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1049 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1050 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1051 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1052 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1053 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1054 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1055 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1056 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1057 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1058 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1059 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1060 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1061 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1062 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1063 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1064 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1065 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1066 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1067 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1068 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1069 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1070 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1071 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1072 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1073 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1074 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1075 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1076 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1077 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1078 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1079 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1080 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1081 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1082 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1083 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1084 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1085 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1086 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1087 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1088 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1089 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1090 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1091 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1092 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1093 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1094 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1095 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1096 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1097 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1098 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1099 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1100 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1101 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1102 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1103 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1104 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1105 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1106 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1107 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1108 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1109 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1110 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1111 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1112 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1113 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1114 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1115 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1116 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1117 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1118 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1119 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1120 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1121 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1122 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1123 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1124 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1125 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1126 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1127 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1128 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1129 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1130 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1131 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1132 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1133 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1134 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1135 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1136 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1137 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1138 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1139 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1140 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1141 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1142 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1143 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1144 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1145 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1146 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1147 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1148 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1149 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1150 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1151 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1152 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1153 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1154 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN W)	12-103						
P1155 HCV	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN							



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GENE	FUNCTION	PROTEIN	FILE NAME	ALL Viruses (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710
PV01	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1	NS1																																																																																																																																																																																																																																																																																																					



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PCGENE	PICTEST2P	ALL Viruses (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PROTEIN	PROTEIN	VARICELLA ZOSTER VIRUS (STRAIN DUMAS)	21-47	154-181	210-212				AREA1
PV01 VACC	PROTEIN 1	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA2
PV01 VACC	PROTEIN 2	VACCINIA VIRUS (STRAIN WA)	89-110						AREA3
PV01 VACC	PROTEIN 3	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA4
PV01 VACC	PROTEIN 4	VACCINIA VIRUS (STRAIN WA)	89-110						AREA5
PV01 VACC	PROTEIN 5	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA6
PV01 VACC	PROTEIN 6	VACCINIA VIRUS (STRAIN WA)	89-110						AREA7
PV01 VACC	PROTEIN 7	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA8
PV01 VACC	PROTEIN 8	VACCINIA VIRUS (STRAIN WA)	89-110						AREA9
PV01 VACC	PROTEIN 9	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA10
PV01 VACC	PROTEIN 10	VACCINIA VIRUS (STRAIN WA)	89-110						AREA11
PV01 VACC	PROTEIN 11	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA12
PV01 VACC	PROTEIN 12	VACCINIA VIRUS (STRAIN WA)	89-110						AREA13
PV01 VACC	PROTEIN 13	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA14
PV01 VACC	PROTEIN 14	VACCINIA VIRUS (STRAIN WA)	89-110						AREA15
PV01 VACC	PROTEIN 15	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA16
PV01 VACC	PROTEIN 16	VACCINIA VIRUS (STRAIN WA)	89-110						AREA17
PV01 VACC	PROTEIN 17	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA18
PV01 VACC	PROTEIN 18	VACCINIA VIRUS (STRAIN WA)	89-110						AREA19
PV01 VACC	PROTEIN 19	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA20
PV01 VACC	PROTEIN 20	VACCINIA VIRUS (STRAIN WA)	89-110						AREA21
PV01 VACC	PROTEIN 21	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA22
PV01 VACC	PROTEIN 22	VACCINIA VIRUS (STRAIN WA)	89-110						AREA23
PV01 VACC	PROTEIN 23	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA24
PV01 VACC	PROTEIN 24	VACCINIA VIRUS (STRAIN WA)	89-110						AREA25
PV01 VACC	PROTEIN 25	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA26
PV01 VACC	PROTEIN 26	VACCINIA VIRUS (STRAIN WA)	89-110						AREA27
PV01 VACC	PROTEIN 27	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA28
PV01 VACC	PROTEIN 28	VACCINIA VIRUS (STRAIN WA)	89-110						AREA29
PV01 VACC	PROTEIN 29	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA30
PV01 VACC	PROTEIN 30	VACCINIA VIRUS (STRAIN WA)	89-110						AREA31
PV01 VACC	PROTEIN 31	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA32
PV01 VACC	PROTEIN 32	VACCINIA VIRUS (STRAIN WA)	89-110						AREA33
PV01 VACC	PROTEIN 33	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA34
PV01 VACC	PROTEIN 34	VACCINIA VIRUS (STRAIN WA)	89-110						AREA35
PV01 VACC	PROTEIN 35	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA36
PV01 VACC	PROTEIN 36	VACCINIA VIRUS (STRAIN WA)	89-110						AREA37
PV01 VACC	PROTEIN 37	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA38
PV01 VACC	PROTEIN 38	VACCINIA VIRUS (STRAIN WA)	89-110						AREA39
PV01 VACC	PROTEIN 39	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA40
PV01 VACC	PROTEIN 40	VACCINIA VIRUS (STRAIN WA)	89-110						AREA41
PV01 VACC	PROTEIN 41	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA42
PV01 VACC	PROTEIN 42	VACCINIA VIRUS (STRAIN WA)	89-110						AREA43
PV01 VACC	PROTEIN 43	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA44
PV01 VACC	PROTEIN 44	VACCINIA VIRUS (STRAIN WA)	89-110						AREA45
PV01 VACC	PROTEIN 45	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA46
PV01 VACC	PROTEIN 46	VACCINIA VIRUS (STRAIN WA)	89-110						AREA47
PV01 VACC	PROTEIN 47	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA48
PV01 VACC	PROTEIN 48	VACCINIA VIRUS (STRAIN WA)	89-110						AREA49
PV01 VACC	PROTEIN 49	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA50
PV01 VACC	PROTEIN 50	VACCINIA VIRUS (STRAIN WA)	89-110						AREA51
PV01 VACC	PROTEIN 51	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA52
PV01 VACC	PROTEIN 52	VACCINIA VIRUS (STRAIN WA)	89-110						AREA53
PV01 VACC	PROTEIN 53	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA54
PV01 VACC	PROTEIN 54	VACCINIA VIRUS (STRAIN WA)	89-110						AREA55
PV01 VACC	PROTEIN 55	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA56
PV01 VACC	PROTEIN 56	VACCINIA VIRUS (STRAIN WA)	89-110						AREA57
PV01 VACC	PROTEIN 57	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA58
PV01 VACC	PROTEIN 58	VACCINIA VIRUS (STRAIN WA)	89-110						AREA59
PV01 VACC	PROTEIN 59	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA60
PV01 VACC	PROTEIN 60	VACCINIA VIRUS (STRAIN WA)	89-110						AREA61
PV01 VACC	PROTEIN 61	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA62
PV01 VACC	PROTEIN 62	VACCINIA VIRUS (STRAIN WA)	89-110						AREA63
PV01 VACC	PROTEIN 63	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA64
PV01 VACC	PROTEIN 64	VACCINIA VIRUS (STRAIN WA)	89-110						AREA65
PV01 VACC	PROTEIN 65	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA66
PV01 VACC	PROTEIN 66	VACCINIA VIRUS (STRAIN WA)	89-110						AREA67
PV01 VACC	PROTEIN 67	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA68
PV01 VACC	PROTEIN 68	VACCINIA VIRUS (STRAIN WA)	89-110						AREA69
PV01 VACC	PROTEIN 69	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA70
PV01 VACC	PROTEIN 70	VACCINIA VIRUS (STRAIN WA)	89-110						AREA71
PV01 VACC	PROTEIN 71	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA72
PV01 VACC	PROTEIN 72	VACCINIA VIRUS (STRAIN WA)	89-110						AREA73
PV01 VACC	PROTEIN 73	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA74
PV01 VACC	PROTEIN 74	VACCINIA VIRUS (STRAIN WA)	89-110						AREA75
PV01 VACC	PROTEIN 75	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA76
PV01 VACC	PROTEIN 76	VACCINIA VIRUS (STRAIN WA)	89-110						AREA77
PV01 VACC	PROTEIN 77	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA78
PV01 VACC	PROTEIN 78	VACCINIA VIRUS (STRAIN WA)	89-110						AREA79
PV01 VACC	PROTEIN 79	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA80
PV01 VACC	PROTEIN 80	VACCINIA VIRUS (STRAIN WA)	89-110						AREA81
PV01 VACC	PROTEIN 81	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA82
PV01 VACC	PROTEIN 82	VACCINIA VIRUS (STRAIN WA)	89-110						AREA83
PV01 VACC	PROTEIN 83	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA84
PV01 VACC	PROTEIN 84	VACCINIA VIRUS (STRAIN WA)	89-110						AREA85
PV01 VACC	PROTEIN 85	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA86
PV01 VACC	PROTEIN 86	VACCINIA VIRUS (STRAIN WA)	89-110						AREA87
PV01 VACC	PROTEIN 87	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA88
PV01 VACC	PROTEIN 88	VACCINIA VIRUS (STRAIN WA)	89-110						AREA89
PV01 VACC	PROTEIN 89	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA90
PV01 VACC	PROTEIN 90	VACCINIA VIRUS (STRAIN WA)	89-110						AREA91
PV01 VACC	PROTEIN 91	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA92
PV01 VACC	PROTEIN 92	VACCINIA VIRUS (STRAIN WA)	89-110						AREA93
PV01 VACC	PROTEIN 93	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA94
PV01 VACC	PROTEIN 94	VACCINIA VIRUS (STRAIN WA)	89-110						AREA95
PV01 VACC	PROTEIN 95	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA96
PV01 VACC	PROTEIN 96	VACCINIA VIRUS (STRAIN WA)	89-110						AREA97
PV01 VACC	PROTEIN 97	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA98
PV01 VACC	PROTEIN 98	VACCINIA VIRUS (STRAIN WA)	89-110						AREA99
PV01 VACC	PROTEIN 99	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA100
PV01 VACC	PROTEIN 100	VACCINIA VIRUS (STRAIN WA)	89-110						AREA101
PV01 VACC	PROTEIN 101	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA102
PV01 VACC	PROTEIN 102	VACCINIA VIRUS (STRAIN WA)	89-110						AREA103
PV01 VACC	PROTEIN 103	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA104
PV01 VACC	PROTEIN 104	VACCINIA VIRUS (STRAIN WA)	89-110						AREA105
PV01 VACC	PROTEIN 105	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA106
PV01 VACC	PROTEIN 106	VACCINIA VIRUS (STRAIN WA)	89-110						AREA107
PV01 VACC	PROTEIN 107	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA108
PV01 VACC	PROTEIN 108	VACCINIA VIRUS (STRAIN WA)	89-110						AREA109
PV01 VACC	PROTEIN 109	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA110
PV01 VACC	PROTEIN 110	VACCINIA VIRUS (STRAIN WA)	89-110						AREA111
PV01 VACC	PROTEIN 111	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA112
PV01 VACC	PROTEIN 112	VACCINIA VIRUS (STRAIN WA)	89-110						AREA113
PV01 VACC	PROTEIN 113	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA114
PV01 VACC	PROTEIN 114	VACCINIA VIRUS (STRAIN WA)	89-110						AREA115
PV01 VACC	PROTEIN 115	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA116
PV01 VACC	PROTEIN 116	VACCINIA VIRUS (STRAIN WA)	89-110						AREA117
PV01 VACC	PROTEIN 117	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA118
PV01 VACC	PROTEIN 118	VACCINIA VIRUS (STRAIN WA)	89-110						AREA119
PV01 VACC	PROTEIN 119	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA120
PV01 VACC	PROTEIN 120	VACCINIA VIRUS (STRAIN WA)	89-110						AREA121
PV01 VACC	PROTEIN 121	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA122
PV01 VACC	PROTEIN 122	VACCINIA VIRUS (STRAIN WA)	89-110						AREA123
PV01 VACC	PROTEIN 123	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA124
PV01 VACC	PROTEIN 124	VACCINIA VIRUS (STRAIN WA)	89-110						AREA125
PV01 VACC	PROTEIN 125	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA126
PV01 VACC	PROTEIN 126	VACCINIA VIRUS (STRAIN WA)	89-110						AREA127
PV01 VACC	PROTEIN 127	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA128
PV01 VACC	PROTEIN 128	VACCINIA VIRUS (STRAIN WA)	89-110						AREA129
PV01 VACC	PROTEIN 129	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA130
PV01 VACC	PROTEIN 130	VACCINIA VIRUS (STRAIN WA)	89-110						AREA131
PV01 VACC	PROTEIN 131	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA132
PV01 VACC	PROTEIN 132	VACCINIA VIRUS (STRAIN WA)	89-110						AREA133
PV01 VACC	PROTEIN 133	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA134
PV01 VACC	PROTEIN 134	VACCINIA VIRUS (STRAIN WA)	89-110						AREA135
PV01 VACC	PROTEIN 135	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA136
PV01 VACC	PROTEIN 136	VACCINIA VIRUS (STRAIN WA)	89-110						AREA137
PV01 VACC	PROTEIN 137	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA138
PV01 VACC	PROTEIN 138	VACCINIA VIRUS (STRAIN WA)	89-110						AREA139
PV01 VACC	PROTEIN 139	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA140
PV01 VACC	PROTEIN 140	VACCINIA VIRUS (STRAIN WA)	89-110						AREA141
PV01 VACC	PROTEIN 141	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA142
PV01 VACC	PROTEIN 142	VACCINIA VIRUS (STRAIN WA)	89-110						AREA143
PV01 VACC	PROTEIN 143	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA144
PV01 VACC	PROTEIN 144	VACCINIA VIRUS (STRAIN WA)	89-110						AREA145
PV01 VACC	PROTEIN 145	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA146
PV01 VACC	PROTEIN 146	VACCINIA VIRUS (STRAIN WA)	89-110						AREA147
PV01 VACC	PROTEIN 147	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA148
PV01 VACC	PROTEIN 148	VACCINIA VIRUS (STRAIN WA)	89-110						AREA149
PV01 VACC	PROTEIN 149	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA150
PV01 VACC	PROTEIN 150	VACCINIA VIRUS (STRAIN WA)	89-110						AREA151
PV01 VACC	PROTEIN 151	VACCINIA VIRUS (STRAIN COPEHAGEN)	89-110						AREA152
PV01 VACC	PROTEIN 152	VACCINIA VIRUS (STRAIN WA)	89-110						AREA153
PV01 VACC	PROTEIN 153	VACCINIA VIRUS							







PCGENE	PICT2ZIP	FILE NAME	PROTEIN	AB Virus (No. Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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[illegible]



GENE			PHITCLIP	AA Virus (No. Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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GENE	FUNCTION	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PVAC1	PROTEIN	171-197								
PVAC2	PROTEIN	171-197								
PVAC3	PROTEIN	171-197								
PVAC4	PROTEIN	171-197								
PVAC5	PROTEIN	171-197								
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PVAC100	PROTEIN	171-197								



ECORDE		FUNCTION		ALL Viruses (No. Bacteriophages)		AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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GENE	FUNCTION	All Viruses (No Serotypes)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 3 / ISOLATE USA)	174-193								
PV1A	STRUCTURAL PROTEIN P1	NEBRASKA CALF DIARRHEA VIRUS (STRAIN NCV-1 LINCOLN)	481-508								
PV1A	STRUCTURAL PROTEIN P1	BOVINE ROTAVIRUS (SEROTYPE 6 / STRAIN B61)	186-207								
PV1A	STRUCTURAL PROTEIN P1	BOVINE ROTAVIRUS (SEROTYPE 6 / STRAIN C486)	481-508								
PV1A	STRUCTURAL PROTEIN P1	BOVINE ROTAVIRUS (STRAIN C486)	481-508								
PV1A	STRUCTURAL PROTEIN P1	EQUINE ROTAVIRUS (STRAIN M-2)	226-249								
PV1A	STRUCTURAL PROTEIN P1	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 10/6)	181-207								
PV1A	STRUCTURAL PROTEIN P1	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-3)	181-207								
PV1A	STRUCTURAL PROTEIN P1	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 69A)	481-508								
PV1A	STRUCTURAL PROTEIN P1	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN DS1)	181-207								
PV1A	STRUCTURAL PROTEIN P1	HUMAN ROTAVIRUS (STRAIN K)	481-508								
PV1A	STRUCTURAL PROTEIN P1	HUMAN ROTAVIRUS (STRAIN KU)	181-207								
PV1A	STRUCTURAL PROTEIN P1	HUMAN ROTAVIRUS (STRAIN L36)	181-207								
PV1A	STRUCTURAL PROTEIN P1	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN M11)	181-207								
PV1A	STRUCTURAL PROTEIN P1	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN MCH1)	181-207								
PV1A	STRUCTURAL PROTEIN P1	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN P)	181-207								
PV1A	STRUCTURAL PROTEIN P1	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST THOMAS 1)	181-207								
PV1A	STRUCTURAL PROTEIN P1	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN VA70)	181-207								
PV1A	STRUCTURAL PROTEIN P1	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	181-207								
PV1A	STRUCTURAL PROTEIN P1	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN OSU)	315-340								
PV1A	STRUCTURAL PROTEIN P1	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	481-508								
PV1A	STRUCTURAL PROTEIN P1	PORCINE ROTAVIRUS (STRAIN GOTTFRIED)	315-340								
PV1A	STRUCTURAL PROTEIN P1	PORCINE ROTAVIRUS (STRAIN YH)	481-508								
PV1A	STRUCTURAL PROTEIN P1	SWINE ROTAVIRUS	481-508								
PV1A	STRUCTURAL PROTEIN P1	SHIGAN 11 ROTAVIRUS (STRAIN SA11-329)	395-411								
PV1A	STRUCTURAL PROTEIN P1	SHIGAN 11 ROTAVIRUS (STRAIN SA11-329)	395-411								
PV1A	STRUCTURAL PROTEIN P1	SOUTHERN BEAN MOSAIC VIRUS	90-114								
PV1A	STRUCTURAL PROTEIN P1	WOUND TUMOR VIRUS	192-215								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	395-411								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	395-411								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	395-411								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	395-411								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE AUSTRALIA)	395-411								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE SOUTH AFRICA)	395-411								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	395-411								
PV1A	STRUCTURAL PROTEIN P1	RICE DWARF VIRUS	262-284								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	6-17								
PV1A	STRUCTURAL PROTEIN P1	AUTOGRAPIA CALIFORNICA NUCLEAR POLYOMYXINOSIS VIRUS	321-337								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	5-23								
PV1A	STRUCTURAL PROTEIN P1	MAIZE ROUGH DWARF VIRUS	190-148								
PV1A	STRUCTURAL PROTEIN P1	ORGYA PSEUDOSUKATA MULTICAUD POLYOMYXINOSIS VIRUS	81-99								
PV1A	STRUCTURAL PROTEIN P1	AUTOGRAPIA CALIFORNICA NUCLEAR POLYOMYXINOSIS VIRUS	84-103								
PV1A	STRUCTURAL PROTEIN P1	GALLERIA MELLONELLA NUCLEAR POLYOMYXINOSIS VIRUS	153-172								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	5-23								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 13 / ISOLATE USA)	5-23								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 13 / ISOLATE USA)	5-23								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 13 / ISOLATE USA)	5-23								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE SOUTH AFRICA)	5-27								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	204-221								
PV1A	STRUCTURAL PROTEIN P1	WOUND TUMOR VIRUS	374-397								
PV1A	STRUCTURAL PROTEIN P1	WOUND TUMOR VIRUS (STRAIN M)	374-397								
PV1A	STRUCTURAL PROTEIN P1	AUTOGRAPIA CALIFORNICA NUCLEAR POLYOMYXINOSIS VIRUS	324-335								
PV1A	STRUCTURAL PROTEIN P1	HEPESVIRUS SAIMIRI (STRAIN 11)	127-147								
PV1A	STRUCTURAL PROTEIN P1	AUTOGRAPIA CALIFORNICA NUCLEAR POLYOMYXINOSIS VIRUS	374-397								
PV1A	STRUCTURAL PROTEIN P1	BLUETONGUE VIRUS (SEROTYPE 13 / ISOLATE USA)	197-215								
PV1A	STRUCTURAL PROTEIN P1	EPIDEMIOLOGICAL DISEASE VIRUS (SEROTYPE 1)	204-222								
PV1A	STRUCTURAL PROTEIN P1	RICE DWARF VIRUS	400-416								
PV1A	STRUCTURAL PROTEIN P1	WOUND TUMOR VIRUS	782-785								



ACCENSE	PICTCLZIP	ALL Viruses (No Bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
PROTEIN	PROTEIN	VIRUS																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															</																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									



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PCORRE	FILE NAME	FUNCTION	PROTEIN	ALL Viruses (No. Bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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294



PCGENE	P1CT2L2IP	All Viruses (No. Bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
BIK-RM16	BIK-RM16	BIK-RM16																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								



REGION	PICTURE	ALL Viruses (No Bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10
AREA 1	PROTEIN	AVIAN ADENOVIRUS GALLI (STRAIN PIHELPS) (POWL ADENOVIRUS 1)	59-10									
AREA 2	PROTEIN	COXSAEVI YELLOW MOTTLE VIRUS	56-51									
AREA 3	PROTEIN	THEMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	13-40									
AREA 4	PROTEIN	COXSAEVI YELLOW MOTTLE VIRUS	23-49									
AREA 5	PROTEIN	EQUINE ARTERITIS VIRUS	165-192									
AREA 6	PROTEIN	LILY STAD VIRUS	196-212									
AREA 7	PROTEIN	LILY VIRUS X	11-92									
AREA 8	PROTEIN	NARCISSUS MOSAIC VIRUS	7-10									
AREA 9	PROTEIN	POTATO VIRUS X	11-34									
AREA 10	PROTEIN	POTATO VIRUS X (STRAIN CP)	11-34									
AREA 11	PROTEIN	WHITE CLOVER MOSAIC VIRUS (STRAIN M)	8-29									
AREA 12	PROTEIN	WHITE CLOVER MOSAIC VIRUS (STRAIN O)	9-31									
AREA 13	PROTEIN	AVIAN ADENOVIRUS GALLI (STRAIN PIHELPS) (POWL ADENOVIRUS 1)	69-86									
AREA 14	PROTEIN	EQUINE ARTERITIS VIRUS	135-138									
AREA 15	PROTEIN	NARCISSUS MOSAIC VIRUS	16-26									
AREA 16	PROTEIN	THEMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	12-32									
AREA 17	PROTEIN	THEMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	16-39									
AREA 18	PROTEIN	THEMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	12-102									
AREA 19	PROTEIN	THEMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1)	91-111									
AREA 20	PROTEIN	PUCE TUNGRU BACILLIFORM VIRUS	2-25									
AREA 21	PROTEIN	PUCE TUNGRU BACILLIFORM VIRUS (ISOLATE PHILIPPINES)	2-25									
AREA 22	PROTEIN	AUTOGRAFIA CALIFORNICA NUCLEAR POLYMERIZATION VIRUS	211-234									
AREA 23	PROTEIN	OROVIRUS PSEUDOTUBULATA MULTICAPSID POLYMERIZATION VIRUS (NP)	12-108									
AREA 24	PROTEIN	OROVIRUS PSEUDOTUBULATA MULTICAPSID POLYMERIZATION VIRUS (NP)	27-34									
AREA 25	PROTEIN	TORRICO NEGROS VIRUS (STRAIN D) (TVV)	12-31									
AREA 26	PROTEIN	LYMANTRIA DISPAR MULTICAPSID NUCLEAR POLYMERIZATION VIRUS	16-35									
AREA 27	PROTEIN	HEAPES SIMPLEX VIRUS (TYPE 6) (STRAIN G3)	42-46									
AREA 28	PROTEIN	HEAPES SIMPLEX VIRUS (TYPE 6) (STRAIN G3)	55-74									
AREA 29	PROTEIN	HEAPES SIMPLEX VIRUS (TYPE 6) (STRAIN G3)	32-54									
AREA 30	PROTEIN	CHILLO INDUCENT VIRUS (CIV) (INSECT INDUCENT VIRUS TYPE 6)	30-41									
AREA 31	PROTEIN	CHILLO INDUCENT VIRUS (CIV) (INSECT INDUCENT VIRUS TYPE 6)	44-49									
AREA 32	PROTEIN	CHILLO INDUCENT VIRUS (CIV) (INSECT INDUCENT VIRUS TYPE 6)	94-123									
AREA 33	PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-1)	199-233									
AREA 34	PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-1)	164-182									
AREA 35	PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-1)	92-113									
AREA 36	PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-1)	137-401									
AREA 37	PROTEIN	OROVIRUS PSEUDOTUBULATA MULTICAPSID POLYMERIZATION VIRUS (NP)	131-152									
AREA 38	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	17-40									
AREA 39	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	12-99									
AREA 40	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	17-40									
AREA 41	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
AREA 42	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
AREA 43	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
AREA 44	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
AREA 45	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
AREA 46	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
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AREA 49	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
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AREA 52	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
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AREA 60	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
AREA 61	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
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AREA 63	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
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AREA 68	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
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AREA 93	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
AREA 94	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
AREA 95	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
AREA 96	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
AREA 97	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
AREA 98	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
AREA 99	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									
AREA 100	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-43									



TABLE XIV

SEARCH RESULTS SUMMARY

FOR P23TLZIPC MOTIF



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[illegible]



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PLC123P	PROTEIN	ALL VIRUSES (see biostriding.org)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PREP CSV	REPEAT ELEMENT PROTEIN	VIRUS	131-109						
PREP CSV	REPEAT ELEMENT PROTEIN	CANINE DISTEMPHER VIRUS (CDV)	14-109						
PREP CSV	REPEAT ELEMENT PROTEIN	BOVINE PARVAVIRUS (BVD)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 1 (EHV-1)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 2 (EHV-2)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 3 (EHV-3)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 4 (EHV-4)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 5 (EHV-5)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 6 (EHV-6)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 7 (EHV-7)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 8 (EHV-8)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 9 (EHV-9)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 10 (EHV-10)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 11 (EHV-11)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 12 (EHV-12)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 13 (EHV-13)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 14 (EHV-14)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 15 (EHV-15)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 16 (EHV-16)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 17 (EHV-17)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 18 (EHV-18)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 19 (EHV-19)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 20 (EHV-20)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 21 (EHV-21)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 22 (EHV-22)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 23 (EHV-23)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 24 (EHV-24)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 25 (EHV-25)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 26 (EHV-26)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 27 (EHV-27)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 28 (EHV-28)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 29 (EHV-29)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 30 (EHV-30)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 31 (EHV-31)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 32 (EHV-32)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 33 (EHV-33)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 34 (EHV-34)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 35 (EHV-35)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 36 (EHV-36)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 37 (EHV-37)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 38 (EHV-38)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 39 (EHV-39)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 40 (EHV-40)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 41 (EHV-41)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 42 (EHV-42)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 43 (EHV-43)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 44 (EHV-44)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 45 (EHV-45)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 46 (EHV-46)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 47 (EHV-47)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 48 (EHV-48)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 49 (EHV-49)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 50 (EHV-50)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 51 (EHV-51)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 52 (EHV-52)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 53 (EHV-53)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 54 (EHV-54)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 55 (EHV-55)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 56 (EHV-56)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 57 (EHV-57)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 58 (EHV-58)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 59 (EHV-59)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 60 (EHV-60)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 61 (EHV-61)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 62 (EHV-62)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 63 (EHV-63)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 64 (EHV-64)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 65 (EHV-65)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 66 (EHV-66)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 67 (EHV-67)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 68 (EHV-68)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 69 (EHV-69)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 70 (EHV-70)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 71 (EHV-71)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 72 (EHV-72)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 73 (EHV-73)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 74 (EHV-74)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 75 (EHV-75)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 76 (EHV-76)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 77 (EHV-77)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 78 (EHV-78)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 79 (EHV-79)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 80 (EHV-80)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 81 (EHV-81)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 82 (EHV-82)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 83 (EHV-83)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 84 (EHV-84)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 85 (EHV-85)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 86 (EHV-86)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 87 (EHV-87)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 88 (EHV-88)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 89 (EHV-89)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 90 (EHV-90)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 91 (EHV-91)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 92 (EHV-92)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 93 (EHV-93)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 94 (EHV-94)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 95 (EHV-95)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 96 (EHV-96)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 97 (EHV-97)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 98 (EHV-98)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 99 (EHV-99)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 100 (EHV-100)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 101 (EHV-101)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 102 (EHV-102)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 103 (EHV-103)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 104 (EHV-104)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 105 (EHV-105)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 106 (EHV-106)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 107 (EHV-107)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 108 (EHV-108)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 109 (EHV-109)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 110 (EHV-110)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 111 (EHV-111)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 112 (EHV-112)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 113 (EHV-113)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 114 (EHV-114)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 115 (EHV-115)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 116 (EHV-116)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 117 (EHV-117)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 118 (EHV-118)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 119 (EHV-119)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 120 (EHV-120)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 121 (EHV-121)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 122 (EHV-122)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 123 (EHV-123)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 124 (EHV-124)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 125 (EHV-125)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 126 (EHV-126)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 127 (EHV-127)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 128 (EHV-128)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 129 (EHV-129)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 130 (EHV-130)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 131 (EHV-131)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 132 (EHV-132)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 133 (EHV-133)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 134 (EHV-134)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 135 (EHV-135)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 136 (EHV-136)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 137 (EHV-137)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 138 (EHV-138)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 139 (EHV-139)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 140 (EHV-140)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 141 (EHV-141)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 142 (EHV-142)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 143 (EHV-143)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 144 (EHV-144)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 145 (EHV-145)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 146 (EHV-146)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 147 (EHV-147)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 148 (EHV-148)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 149 (EHV-149)	44-19						
PREP CSV	REPEAT ELEMENT PROTEIN	EQUINE HERPESVIRUS TYPE 150 (EHV-150)	44-19						



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[illegible]



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[illegible]



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[illegible]



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[illegible]



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[illegible]



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[illegible]



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[illegible]



[illegible]



TABLE XV  
RESPIRATORY SYNCYTIAL VIRUS DP107 F2 REGION ANALOG  
CARBOXY TRUNCATIONS

X-YTS-Z  
 X-YTSV-Z  
 5 X-YTSVI-Z  
 X-YTSVIT-Z  
 X-YTSVITI-Z  
 X-YTSVITIE-Z  
 X-YTSVITIEL-Z  
 X-YTSVITIELS-Z  
 X-YTSVITIELSN-Z  
 10 X-YTSVITIELSNI-Z  
 X-YTSVITIELSNIK-Z  
 X-YTSVITIELSNIKE-Z  
 X-YTSVITIELSNIKEN-Z  
 X-YTSVITIELSNIKENK-Z  
 X-YTSVITIELSNIKENKC-Z  
 X-YTSVITIELSNIKENKCN-Z  
 X-YTSVITIELSNIKENKCNG-Z  
 15 X-YTSVITIELSNIKENKCNGT-Z  
 X-YTSVITIELSNIKENKCNGTD-Z  
 X-YTSVITIELSNIKENKCNGTDA-Z  
 X-YTSVITIELSNIKENKCNGTDAK-Z  
 X-YTSVITIELSNIKENKCNGTDAKV-Z  
 X-YTSVITIELSNIKENKCNGTDAKVK-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKL-Z  
 20 X-YTSVITIELSNIKENKCNGTDAKVKLI-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIK-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQ-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQE-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQEL-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDK-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKY-Z  
 25 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYK-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKN-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNA-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAV-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTE-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTEL-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQ-Z  
 30 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQL-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLL-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLM-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQ-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQS-Z  
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z

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The one letter amino acid code is used.



Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxycarbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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**TABLE XVI**  
**RESPIRATORY SYNCYTIAL VIRUS F2 DP178/DP107 REGION ANALOG**  
**AMINO TRUNCATIONS**

	X-QST-Z
	X-MQST-Z
5	X-LMQST-Z
	X-LLMQST-Z
	X-QLLMQST-Z
	X-LQLLMQST-Z
	X-ELQLLMQST-Z
	X-TELQLLMQST-Z
	X-VTELQLLMQST-Z
10	X-AVTELQLLMQST-Z
	X-NAVTELQLLMQST-Z
	X-KNAVTELQLLMQST-Z
	X-YKNAVTELQLLMQST-Z
	X-KYKNAVTELQLLMQST-Z
	X-DKYKNAVTELQLLMQST-Z
	X-LDKYKNAVTELQLLMQST-Z
15	X-ELDKYKNAVTELQLLMQST-Z
	X-QELDKYKNAVTELQLLMQST-Z
	X-KQELDKYKNAVTELQLLMQST-Z
	X-IKQELDKYKNAVTELQLLMQST-Z
	X-LIKQELDKYKNAVTELQLLMQST-Z
	X-KLIKQELDKYKNAVTELQLLMQST-Z
	X-VKLIKQELDKYKNAVTELQLLMQST-Z
	X-KVKLIKQELDKYKNAVTELQLLMQST-Z
20	X-AKVLIKQELDKYKNAVTELQLLMQST-Z
	X-DAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-TDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-GTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-CNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-KCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
25	X-NKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-KENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-IKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-SNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-LSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-ELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-IELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
30	X-TIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-ITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-VITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-SVITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-TSVITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z

The one letter amino acid code is used.

35 Additionally,



"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVII  
RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG  
CARBOXY TRUNCATIONS

	X-FYD-Z
	X-FYDP-Z
	X-FYDPL-Z
5	X-FYDPLV-Z
	X-FYDPLVF-Z
	X-FYDPLVFP-Z
	X-FYDPLVFPS-Z
	X-FYDPLVFPSD-Z
	X-FYDPLVFPSDE-Z
	X-FYDPLVFPSDEF-Z
10	X-FYDPLVFPSDEFD-Z
	X-FYDPLVFPSDEFDA-Z
	X-FYDPLVFPSDEFDAS-Z
	X-FYDPLVFPSDEFDASI-Z
	X-FYDPLVFPSDEFDASIS-Z
	X-FYDPLVFPSDEFDASISQ-Z
	X-FYDPLVFPSDEFDASISQV-Z
	X-FYDPLVFPSDEFDASISQVN-Z
15	X-FYDPLVFPSDEFDASISQVNE-Z
	X-FYDPLVFPSDEFDASISQVNEK-Z
	X-FYDPLVFPSDEFDASISQVNEKI-Z
	X-FYDPLVFPSDEFDASISQVNEKIN-Z
	X-FYDPLVFPSDEFDASISQVNEKINQ-Z
	X-FYDPLVFPSDEFDASISQVNEKINQS-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSL-Z
20	X-FYDPLVFPSDEFDASISQVNEKINQSLA-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFI-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIR-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRK-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKS-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSD-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDE-Z
25	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDEL-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier



group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVIII  
RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG  
AMINO TRUNCATIONS

	X-DELL-Z
	X-SDELL-Z
5	X-KSDELL-Z
	X-RKSDELL-Z
	X-IRKSDELL-Z
	X-FIRKSDELL-Z
	X-AFIRKSDELL-Z
	X-LAFIRKSDELL-Z
	X-SLAFIRKSDELL-Z
10	X-QSLAFIRKSDELL-Z
	X-NQSLAFIRKSDELL-Z
	X-INQSLAFIRKSDELL-Z
	X-KINQSLAFIRKSDELL-Z
	X-EKINQSLAFIRKSDELL-Z
	X-NEKINQSLAFIRKSDELL-Z
	X-VNEKINQSLAFIRKSDELL-Z
	X-QVNEKINQSLAFIRKSDELL-Z
15	X-SQVNEKINQSLAFIRKSDELL-Z
	X-ISQVNEKINQSLAFIRKSDELL-Z
	X-SISQVNEKINQSLAFIRKSDELL-Z
	X-ASISQVNEKINQSLAFIRKSDELL-Z
	X-DASISQVNEKINQSLAFIRKSDELL-Z
	X-FDASISQVNEKINQSLAFIRKSDELL-Z
	X-EFDASISQVNEKINQSLAFIRKSDELL-Z
20	X-DEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-SDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-PSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-FPSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-VFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-LVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-PLVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-DPLVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z
25	X-YDPLVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.



TABLE XIX  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG  
CARBOXY TRUNCATIONS

X-ITL-Z  
 X-ITLN-Z  
 X-ITLNN-Z  
 5 X-ITLNNNS-Z  
 X-ITLNNNSV-Z  
 X-ITLNNNSVA-Z  
 X-ITLNNNSVAL-Z  
 X-ITLNNNSVALD-Z  
 X-ITLNNNSVALDP-Z  
 X-ITLNNNSVALDPID-Z  
 10 X-ITLNNNSVALDPIDI-Z  
 X-ITLNNNSVALDPIDIS-Z  
 X-ITLNNNSVALDPIDISI-Z  
 X-ITLNNNSVALDPIDISIE-Z  
 X-ITLNNNSVALDPIDISIEL-Z  
 X-ITLNNNSVALDPIDISIELN-Z  
 X-ITLNNNSVALDPIDISIELNK-Z  
 15 X-ITLNNNSVALDPIDISIELNKA-Z  
 X-ITLNNNSVALDPIDISIELNKAK-Z  
 X-ITLNNNSVALDPIDISIELNKAKS-Z  
 X-ITLNNNSVALDPIDISIELNKAKSD-Z  
 X-ITLNNNSVALDPIDISIELNKAKSDL-Z  
 X-ITLNNNSVALDPIDISIELNKAKSDLE-Z  
 X-ITLNNNSVALDPIDISIELNKAKSDLEE-Z  
 20 X-ITLNNNSVALDPIDISIELNKAKSDLEES-Z  
 X-ITLNNNSVALDPIDISIELNKAKSDLEESK-Z  
 X-ITLNNNSVALDPIDISIELNKAKSDLEESKE-Z  
 X-ITLNNNSVALDPIDISIELNKAKSDLEESKEW-Z  
 X-ITLNNNSVALDPIDISIELNKAKSDLEESKEWI-Z  
 X-ITLNNNSVALDPIDISIELNKAKSDLEESKEWIR-Z  
 X-ITLNNNSVALDPIDISIELNKAKSDLEESKEWIRR-Z  
 25 X-ITLNNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxy, dansyl, or  
 T-butyloxycarbonyl; an acetyl group; a 9-  
 30 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
 T-butyloxycarbonyl group; a macromolecular carrier  
 group including but not limited to lipid-fatty acid  
 35 conjugates, polyethylene glycol, or carbohydrates.



TABLE XX  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG  
AMINO TRUNCATIONS

	X-RRS-Z
	X-IRRS-Z
5	X-WIRRS-Z
	X-EWIRRS-Z
	X-KEWIRRS-Z
	X-SKEWIRRS-Z
	X-ESKEWIRRS-Z
	X-EESKEWIRRS-Z
	X-LEESKEWIRRS-Z
10	X-DLEESKEWIRRS-Z
	X-SDLEESKEWIRRS-Z
	X-KSDLEESKEWIRRS-Z
	X-AKSDLEESKEWIRRS-Z
	X-KAKSDLEESKEWIRRS-Z
	X-NKAKSDLEESKEWIRRS-Z
	X-LNKAKSDLEESKEWIRRS-Z
	X-ELNKAKSDLEESKEWIRRS-Z
15	X-IELNKAKSDLEESKEWIRRS-Z
	X-SIELNKAKSDLEESKEWIRRS-Z
	X-ISIELNKAKSDLEESKEWIRRS-Z
	X-DISIELNKAKSDLEESKEWIRRS-Z
	X-IDISIELNKAKSDLEESKEWIRRS-Z
	X-PIDISIELNKAKSDLEESKEWIRRS-Z
	X-DPIDISIELNKAKSDLEESKEWIRRS-Z
20	X-LDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-ALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-VALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-SVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-NSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-NNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-LNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
25	X-TLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a  
 30 macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid  
 35 conjugates, polyethylene glycol, or carbohydrates.



TABLE XXI  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG  
CARBOXY TRUNCATIONS

- X-ALG-Z  
 X-ALGV-Z  
 X-ALGVA-Z  
 5 X-ALGVAT-Z  
 X-ALGVATS-Z  
 X-ALGVATSA-Z  
 X-ALGVATSAQ-Z  
 X-ALGVATSAQI-Z  
 X-ALGVATSAQIT-Z  
 X-ALGVATSAQITA-Z  
 10 X-ALGVATSAQITAA-Z  
 X-ALGVATSAQITA-AV-Z  
 X-ALGVATSAQITA-AVA-Z  
 X-ALGVATSAQITA-AVAL-Z  
 X-ALGVATSAQITA-AVALV-Z  
 X-ALGVATSAQITA-AVALVE-Z  
 X-ALGVATSAQITA-AVALVEA-Z  
 X-ALGVATSAQITA-AVALVEAK-Z  
 15 X-ALGVATSAQITA-AVALVEAKQ-Z  
 X-ALGVATSAQITA-AVALVEAKQA-Z  
 X-ALGVATSAQITA-AVALVEAKQAR-Z  
 X-ALGVATSAQITA-AVALVEAKQARS-Z  
 X-ALGVATSAQITA-AVALVEAKQARSD-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDI-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIE-Z  
 20 X-ALGVATSAQITA-AVALVEAKQARSDIEKL-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLK-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLKE-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLKEA-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLKEAI-Z  
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLKEAIR-Z
- 25 The one letter amino acid code is used.

Additionally,

- "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a  
 30 macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XXII  
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG  
AMINO TRUNCATIONS

	X-IRD-Z
	X-AIRD-Z
5	X-EAIRD-Z
	X-KEAIRD-Z
	X-LKEAIRD-Z
	X-KLKEAIRD-Z
	X-EKLKEAIRD-Z
	X-IEKLKEAIRD-Z
	X-DIEKLKEAIRD-Z
10	X-SDIEKLKEAIRD-Z
	X-RSDIEKLKEAIRD-Z
	X-ARSDIEKLKEAIRD-Z
	X-QARSDIEKLKEAIRD-Z
	X-KQARSDIEKLKEAIRD-Z
	X-AKQARSDIEKLKEAIRD-Z
	X-EAKQARSDIEKLKEAIRD-Z
	X-VEAKQARSDIEKLKEAIRD-Z
15	X-LVEAKQARSDIEKLKEAIRD-Z
	X-ALVEAKQARSDIEKLKEAIRD-Z
	X-VALVEAKQARSDIEKLKEAIRD-Z
	X-AVALVEAKQARSDIEKLKEAIRD-Z
	X-AAVALVEAKQARSDIEKLKEAIRD-Z
	X-TAAVALVEAKQARSDIEKLKEAIRD-Z
	X-ITAVALVEAKQARSDIEKLKEAIRD-Z
20	X-QITAVALVEAKQARSDIEKLKEAIRD-Z
	X-AQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-SAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-TSAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-ATSAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-VATSAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-GVATSAQITAVALVEAKQARSDIEKLKEAIRD-Z
25	X-LGVATSAQITAVALVEAKQARSDIEKLKEAIRD-Z

The one letter amino acid code is used.

Additionally,  
 "X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxy, dansyl, or  
 T-butyloxycarbonyl; an acetyl group; a 9-  
 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 30 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a  
 T-butyloxycarbonyl group; a macromolecular carrier  
 group including but not limited to lipid-fatty acid  
 35 conjugates, polyethylene glycol, or carbohydrates.



TABLE XXIII  
REPRESENTATIVE DP107/DP178 ANALOG ANTIVIRAL PEPTIDES

Anti-Respiratory syncytial virus peptides

- X-TSVITIELSNIKENKCNCTDAKVLIKQELDKYKN-Z  
 X-SVITIELSNIKENKCNCTDAKVLIKQELDKYKNA-Z  
 5 X-VITIELSNIKENKCNCTDAKVLIKQELDKYKNAV-Z  
 X-VAVSKVLHLEGEVNKIALSTNKAVVSLSNGVS-Z  
 X-AVSKVLHLEGEVNKIALSTNKAVVSLSNGVSV-Z  
 X-VSKVLHLEGEVNKIALSTNKAVVSLSNGVSVL-Z  
 X-SKVLHLEGEVNKIALSTNKAVVSLSNGVSVLT-Z  
 X-KVLHLEGEVNKIALSTNKAVVSLSNGVSVLTS-Z  
 X-LEGEVNKIALSTNKAVVSLSNGVSVLTSKVLD-Z  
 10 X-GEVNKIALSTNKAVVSLSNGVSVLTSKVLDLK-Z  
 X-EVNKIALSTNKAVVSLSNGVSVLTSKVLDLKN-Z  
 X-VNKIALSTNKAVVSLSNGVSVLTSKVLDLKNY-Z  
 X-NKIALSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z  
 X-KIALSTNKAVVSLSNGVSVLTSKVLDLKNYID-Z  
 X-IALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z  
 X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQ-Z  
 X-VAVSKVLHLEGEVNKIALSTNKAVVSLSNGVS-Z  
 15 X-AVSKVLHLEGEVNKIALSTNKAVVSLSNGVSV-Z  
 X-VSKVLHLEGEVNKIALSTNKAVVSLSNGVSVL-Z  
 X-SKVLHLEGEVNKIALSTNKAVVSLSNGVSVLT-Z  
 X-KVLHLEGEVNKIALSTNKAVVSLSNGVSVLTS-Z  
 X-LEGEVNKIALSTNKAVVSLSNGVSVLTSKVLD-Z  
 X-GEVNKIALSTNKAVVSLSNGVSVLTSKVLDLK-Z  
 X-EVNKIALSTNKAVVSLSNGVSVLTSKVLDLKN-Z  
 20 X-VNKIALSTNKAVVSLSNGVSVLTSKVLDLKNY-Z  
 X-NKIALSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z  
 X-KIALSTNKAVVSLSNGVSVLTSKVLDLKNYID-Z  
 X-IALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z  
 X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQ-Z

Anti-human parainfluenza virus 3 peptides

- 25 X-TLNNSVALDPIDISIELNKAQSDLEESKEWIRRSN-Z  
 X-LNNSVALDPIDISIELNKAQSDLEESKEWIRRSNQ-Z  
 X-NNSVALDPIDISIELNKAQSDLEESKEWIRRSNQK-Z  
 X-NSVALDPIDISIELNKAQSDLEESKEWIRRSNQKL-Z  
 X-SVALDPIDISIELNKAQSDLEESKEWIRRSNQKLD-Z  
 X-VALDPIDISIELNKAQSDLEESKEWIRRSNQKLDZ-Z  
 X-ALDPIDISIELNKAQSDLEESKEWIRRSNQKLDZS-Z  
 30 X-LDPIDISIELNKAQSDLEESKEWIRRSNQKLDZSIG-Z  
 X-DPIDISIELNKAQSDLEESKEWIRRSNQKLDZSIGN-Z  
 X-PIDISIELNKAQSDLEESKEWIRRSNQKLDZSIGNW-Z  
 X-IDISIELNKAQSDLEESKEWIRRSNQKLDZSIGNWH-Z  
 X-DISIELNKAQSDLEESKEWIRRSNQKLDZSIGNWHQ-Z  
 X-ISIELNKAQSDLEESKEWIRRSNQKLDZSIGNWHQS-Z  
 X-SIELNKAQSDLEESKEWIRRSNQKLDZSIGNWHQSS-Z  
 X-IELNKAQSDLEESKEWIRRSNQKLDZSIGNWHQSST-Z  
 35 X-ELNKAQSDLEESKEWIRRSNQKLDZSIGNWHQSSTT-Z  
 X-TAAVALVEAKQARSIDIEKLKEAIRDTNKAVQSVQS-Z



X-AVALVEAKQARSDIEKLKEAIRD TNKAVQSVQSSI-Z  
 X-LVEAKQARSDIEKLKEAIRD TNKAVQSVQSSIGNL-Z  
 X-VEAKQARSDIEKLKEAIRD TNKAVQSVQSSIGNLI-Z  
 X-EAKQARSDIEKLKEAIRD TNKAVQSVQSSIGNLIV-Z  
 X-AKQARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVA-Z  
 X-KQARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAI-Z  
 X-QARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIK-Z  
 5 X-ARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIKS-Z  
 X-RSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIKSV-Z  
 X-SDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIKSVQ-Z  
 X-KLKEAIRD TNKAVQSVQSSIGNLIVAIKSVQDYVN-Z  
 X-LKEAIRD TNKAVQSVQSSIGNLIVAIKSVQDYVVK-Z  
 X-AIRD TNKAVQSVQSSIGNLIVAIKSVQDYVNKEIV-Z

10 Anti-simian immunodeficiency virus peptides

X-WQEWERKVD FLEENITALLEEAQIQQEK NMYELQK-Z  
 X-QEWERKVD FLEENITALLEEAQIQQEK NMYELQKL-Z  
 X-EWERKVD FLEENITALLEEAQIQQEK NMYELQKLN-Z  
 X-WERKVD FLEENITALLEEAQIQQEK NMYELQKLNS-Z  
 X-ERKVD FLEENITALLEEAQIQQEK NMYELQKLNSW-Z  
 X-RKVD FLEENITALLEEAQIQQEK NMYELQKLNSWD-Z  
 15 X-KVD FLEENITALLEEAQIQQEK NMYELQKLNSWDV-Z  
 X-VDFLEENITALLEEAQIQQEK NMYELQKLNSWDVF-Z  
 X-DFLEENITALLEEAQIQQEK NMYELQKLNSWDVFG-Z  
 X-FLEENITALLEEAQIQQEK NMYELQKLNSWDVFGN-Z

Anti-measles virus peptides

20 X-LHRIDLGPPI SLERLDVGTNLGN AIAKLEAKELL-Z  
 X-HRIDLGPPI SLERLDVGTNLGN AIAKLEAKELLE-Z  
 X-RIDLGPPI SLERLDVGTNLGN AIAKLEAKELLES-Z  
 X-IDLGPPI SLERLDVGTNLGN AIAKLEAKELLESS-Z  
 X-DLGPPI SLERLDVGTNLGN AIAKLEAKELLESSD-Z  
 X-LGPPI SLERLDVGTNLGN AIAKLEAKELLESSDQ-Z  
 X-GPPI SLERLDVGTNLGN AIAKLEAKELLESSDQI-Z  
 25 X-PPISLERLDVGTNLGN AIAKLEAKELLESSDQIL-Z  
 X-PISLERLDVGTNLGN AIAKLEAKELLESSDQILR-Z  
 X-SLERLDVGTNLGN AIAKLEAKELLESSDQILRSM-Z  
 X-LERLDVGTNLGN AIAKLEAKELLESSDQILRSMK-Z

The one letter amino acid code is used.

30 Additionally,  
 "X" may represent an amino group, a hydrophobic group,  
 including but not limited to carbobenzoxyl, dansyl, or  
 T-butyloxycarbonyl; an acetyl group; a 9-  
 fluorenylmethoxy-carbonyl (Fmoc) group; a  
 macromolecular carrier group including but not limited  
 to lipid-fatty acid conjugates, polyethylene glycol,  
 or carbohydrates.  
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"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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#### 5.4. SYNTHESIS OF PEPTIDES

The peptides of the invention may be synthesized or prepared by techniques well known in the art. See, for example, Creighton, 1983, Proteins: Structures  
5 and Molecular Principles, W.H. Freeman and Co., NY, which is incorporated herein by reference in its entirety. Short peptides, for example, can be synthesized on a solid support or in solution. Longer peptides may be made using recombinant DNA techniques.  
10 Here, the nucleotide sequences encoding the peptides of the invention may be synthesized, and/or cloned, and expressed according to techniques well known to those of ordinary skill in the art. See, for example, Sambrook, et al., 1989, Molecular Cloning, A  
15 Laboratory Manual, Vols. 1-3, Cold Spring Harbor Press, NY.

The peptides of the invention may alternatively be synthesized such that one or more of the bonds which link the amino acid residues of the peptides are  
20 non-peptide bonds. These alternative non-peptide bonds may be formed by utilizing reactions well known to those in the art, and may include, but are not limited to imino, ester, hydrazide, semicarbazide, and azo bonds, to name but a few. In yet another  
25 embodiment of the invention, peptides comprising the sequences described above may be synthesized with additional chemical groups present at their amino and/or carboxy termini, such that, for example, the stability, bioavailability, and/or inhibitory activity  
30 of the peptides is enhanced. For example, hydrophobic groups such as carbobenzoxyl, dansyl, or t-butyloxycarbonyl groups, may be added to the peptides' amino termini. Likewise, an acetyl group or a 9-fluorenylmethoxy-carbonyl group may be placed at the  
35 peptides' amino termini. (See "X" in Tables I to IV,



above.) Additionally, the hydrophobic group, t-butyloxycarbonyl, or an amido group may be added to the peptides' carboxy termini. (See "Z" in Tables I to IV, above.)

5 Further, the peptides of the invention may be synthesized such that their steric configuration is altered. For example, the D-isomer of one or more of the amino acid residues of the peptide may be used, rather than the usual L-isomer.

10 Still further, at least one of the amino acid residues of the peptides of the invention may be substituted by one of the well known non-naturally occurring amino acid residues. Alterations such as these may serve to increase the stability, bioavailability and/or inhibitory action of the  
15 peptides of the invention.

Any of the peptides described above may, additionally, have a macromolecular carrier group covalently attached to their amino and/or carboxy termini. Such macromolecular carrier groups may  
20 include, for example, lipid-fatty acid conjugates, polyethylene glycol, carbohydrates or additional peptides. "X", in Tables I to IV, above, may therefore additionally represent any of the above macromolecular carrier groups covalently attached to  
25 the amino terminus of a peptide, with an additional peptide group being preferred. Likewise, "Z", in Tables I to IV, may additionally represent any of the macromolecular carrier groups described above.

30 5.5. ASSAYS FOR ANTI-MEMBRANE FUSION ACTIVITY

Described herein, are methods for ability of a compound, such as the peptides of the invention, to inhibit membrane fusion events. Specifically, assays for cell fusion events are described in Section 5.5.1,  
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below, and assays for antiviral activity are described in Section 5.5.2, below.

#### 5.5.1 ASSAYS FOR CELL FUSION EVENTS

Assays for cell fusion events are well known to those of skill in the art, and may be used in conjunction, for example, with the peptides of the invention to test the peptides' antifusogenic capabilities.

Cell fusion assays are generally performed in vitro. Such an assay may comprise culturing cells which, in the absence of any treatment would undergo an observable level of syncytial formation. For example, uninfected cells may be incubated in the presence of cells chronically infected with a virus that induces cell fusion. Such viruses may include, but are not limited to, HIV, SIV, or respiratory syncytial virus.

For the assay, cells are incubated in the presence of a peptide to be assayed. For each peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added.

Standard conditions for culturing cells, well known to those of ordinary skill in the art, are used. After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytial formation. Well known stains, such as crystal violet stain, may be used to facilitate the visualization of syncytial formation.

#### 5.5.2 ASSAYS FOR ANTIVIRAL ACTIVITY

The antiviral activity exhibited by the peptides of the invention may be measured, for example, by



easily performed in vitro assays, such as those described below, which can test the peptides' ability to inhibit syncytia formation, or their ability to inhibit infection by cell-free virus. Using these assays, such parameters as the relative antiviral activity of the peptides, exhibit against a given strain of virus and/or the strain specific inhibitory activity of the peptide can be determined.

A cell fusion assay may be utilized to test the peptides' ability to inhibit viral-induced, such as HIV-induced, syncytia formation in vitro. Such an assay may comprise culturing uninfected cells in the presence of cells chronically infected with a syncytial-inducing virus and a peptide to be assayed. For each peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added. Standard conditions for culturing, well known to those of ordinary skill in the art, are used. After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytia formation. Well known stains, such as crystal violet stain, may be used to facilitate syncytial visualization. Taking HIV as an example, such an assay would comprise CD-4<sup>+</sup> cells (such as Molt or CEM cells, for example) cultured in the presence of chronically HIV-infected cells and a peptide to be assayed.

Other well known characteristics of viral infection may also be assayed to test a peptide's antiviral capabilities. Once again taking HIV as an example, a reverse transcriptase (RT) assay may be utilized to test the peptides' ability to inhibit infection of CD-4<sup>+</sup> cells by cell-free HIV. Such an assay may comprise culturing an appropriate



concentration (i.e., TCID<sub>50</sub>) of virus and CD-4<sup>+</sup> cells in the presence of the peptide to be tested. Culture conditions well known to those in the art are used. As above, a range of peptide concentrations may be used, in addition to a control culture wherein no peptide has been added. After incubation for an appropriate period (e.g., 7 days) of culturing, a cell-free supernatant is prepared, using standard procedures, and tested for the presence of RT activity as a measure of successful infection. The RT activity may be tested using standard techniques such as those described by, for example, Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and/or Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). These references are incorporated herein by reference in their entirety.

Standard methods which are well-known to those of skill in the art may be utilized for assaying non-retroviral activity. See, for example, Pringle et al. (Pringle, C.R. et al., 1985, J. Medical Virology 17:377-386) for a discussion of respiratory syncytial virus and parainfluenza virus activity assay techniques. Further, see, for example, "Zinsser Microbiology", 1988, Joklik, W.K. et al., eds., Appleton & Lange, Norwalk, CT, 19th ed., for a general review of such techniques. These references are incorporated by reference herein in their entirety. In addition, the Examples presented below, in Sections 17, 18, 26 and 27 each provide additional assays for the testing of a compound's antiviral capability.

In vivo assays may also be utilized to test, for example, the antiviral activity of the peptides of the invention. To test for anti-HIV activity, for example, the in vivo model described in Barnett et al. (Barnett, S.W. et al., 1994, Science 266:642-646) may be used.



Additionally, anti-RSV activity can be assayed in vivo via well known mouse models. For example, RSV can be administered intranasally to mice of various inbred strains. Virus replicates in lungs of all strains, but the highest titers are obtained in P/N, C57L/N and DBA/2N mice. Infection of BALB/c mice produces an asymptomatic bronchiolitis characterized by lymphocytic infiltrates and pulmonary virus titers of  $10^4$  to  $10^5$  pfu/g of lung tissue (Taylor, G. et al., 1984, Infect. Immun. 43:649-655).

Cotton rat models of RSV are also well known. Virus replicates to high titer in the nose and lungs of the cotton rat but produces few if any signs of inflammation.

#### 5.6. USES OF THE PEPTIDES OF THE INVENTION

The peptides of the invention may be utilized as antifusogenic or antiviral compounds, or as compounds which modulate intracellular processes involving coiled coil peptide structures. Further, such peptides may be used to identify agents which exhibit antifusogenic, antiviral or intracellular modulatory activity. Still further, the peptides of the invention may be utilized as organism or viral type/subtype-specific diagnostic tools.

The antifusogenic capability of the peptides of the invention may additionally be utilized to inhibit or treat/ameliorate symptoms caused by processes involving membrane fusion events. Such events may include, for example, virus transmission via cell-cell fusion, abnormal neurotransmitter exchange via cell-fusion, and sperm-egg fusion. Further, the peptides of the invention may be used to inhibit free viral, such as retroviral, particularly HIV, transmission to uninfected cells wherein such viral infection involves membrane fusion events or involves fusion of a viral



structure with a cell membrane. Among the intracellular disorders involving coiled coil peptides structures which may be ameliorated by the peptides of the invention are disorders involving, for example, bacterial toxins.

5 With respect to antiviral activity, the viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to all strains of the viruses listed above, in Tables V through VII, and IX through XIV.

10 These viruses include, for example, human retroviruses, particularly HIV-1 and HIV-2 and the human T-lymphocyte viruses (HTLV-I and II). The non-human retroviruses whose transmission may be inhibited by the peptides of the invention include, but are not  
15 limited to bovine leukosis virus, feline sarcoma and leukemia viruses, simian immunodeficiency, sarcoma and leukemia viruses, and sheep progress pneumonia viruses.

Non retroviral viruses whose transmission may be  
20 inhibited by the peptides of the invention include, but are not limited to human respiratory syncytial virus, canine distemper virus, newcastle disease virus, human parainfluenza virus, influenza viruses, measles viruses, Epstein-Barr viruses, hepatitis B  
25 viruses, and simian Mason-Pfizer viruses.

Non enveloped viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to picornaviruses such as polio viruses, hepatitis A virus, enterovirus, echoviruses  
30 and coxsackie viruses, papovaviruses such as papilloma virus, parvoviruses, adenoviruses and reoviruses.

As discussed more fully, below, in Section 5.5.1 and in the Example presented, below, in Section 8, DP107, DP178, DP107 analog and DP178 analog peptides  
35 form non-covalent protein-protein interactions which



are required for normal activity of the virus. Thus, the peptides of the invention may also be utilized as components in assays for the identification of compounds that interfere with such protein-protein interactions and may, therefore, act as antiviral agents. These assays are discussed, below, in Section 5.5.1.

As demonstrated in the Example presented below in Section 6, the antiviral activity of the peptides of the invention may show a pronounced type and subtype specificity, i.e., specific peptides may be effective in inhibiting the activity of only specific viruses. This feature of the invention presents many advantages. One such advantage, for example, lies in the field of diagnostics, wherein one can use the antiviral specificity of the peptide of the invention to ascertain the identity of a viral isolate. With respect to HIV, one may easily determine whether a viral isolate consists of an HIV-1 or HIV-2 strain. For example, uninfected CD-4<sup>+</sup> cells may be co-infected with an isolate which has been identified as containing HIV the DP178 (SEQ ID:1) peptide, after which the retroviral activity of cell supernatants may be assayed, using, for example, the techniques described above in Section 5.2. Those isolates whose retroviral activity is completely or nearly completely inhibited contain HIV-1. Those isolates whose viral activity is unchanged or only reduced by a small amount, may be considered to not contain HIV-1. Such an isolate may then be treated with one or more of the other DP178 peptides of the invention, and subsequently be tested for its viral activity in order to determine the identify of the viral isolate. The DP107 and DP178 analogs of the invention may also be utilized in a diagnostic capacity specific to the type and subtype of virus or organism in which the specific



peptide sequence is found. A diagnostic procedure as described, above, for DP178, may be used in conjunction with the DP107/DP178 analog of interest.

#### 5.5.1. SCREENING ASSAYS

5 As demonstrated in the Example presented in Section 8, below, DP107 and DP178 portions of the TM protein gp41 form non-covalent protein-protein interactions. As is also demonstrated, the maintenance of such interactions is necessary for  
10 normal viral infectivity. Thus, compounds which bind DP107, bind DP178, and/or act to disrupt normal DP107/DP178 protein-protein interactions may act as antifusogenic, antiviral or cellular modulatory agents. Described below are assays for the  
15 identification of such compounds. Note that, while, for ease and clarity of discussion, DP107 and DP178 peptides will be used as components of the assays described, but it is to be understood that any of the DP107 analog or DP178 analog peptides described,  
20 above, in Sections 5.1 through 5.3 may also be utilized as part of these screens for compounds.

Compounds which may be tested for an ability to bind DP107, DP178, and/or disrupt DP107/DP178 interactions, and which therefore, potentially  
25 represent antifusogenic, antiviral or intracellular modulatory compounds, include, but are not limited to, peptides made of D- and/or L-configuration amino acids (in, for example, the form of random peptide libraries; see Lam, K.S. et al., 1991, Nature 354:82-  
30 84), phosphopeptides (in, for example, the form of random or partially degenerate, directed phosphopeptide libraries; see, for example, Songyang, Z. et al., 1993, Cell 72:767-778), antibodies, and small organic or inorganic molecules. Synthetic  
35 compounds, natural products, and other sources of



potentially effective materials may be screened in a variety of ways, as described in this Section.

The compounds, antibodies, or other molecules identified may be tested, for example, for an ability to inhibit cell fusion or viral activity, utilizing, for example, assays such as those described, above, in Section 5.5.

Among the peptides which may be tested are soluble peptides comprising DP107 and/or DP178 domains, and peptides comprising DP107 and/or DP178 domains having one or more mutations within one or both of the domains, such as the M41-P peptide described, below, in the Example presented in Section 8, which contains a isoleucine to proline mutation within the DP178 sequence.

In one embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

(a) exposing at least one compound to a peptide comprising a DP107 peptide for a time sufficient to allow binding of the compound to the DP107 peptide;

(b) removing non-bound compounds; and

(c) determining the presence of the compound bound to the DP107 peptide, thereby identifying an agent to be tested for antiviral ability.

In a second embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

(a) exposing at least one compound to a peptide comprising a DP178 peptide for a time sufficient to allow binding of the compound to the DP178 peptide;

(b) removing non-bound compounds; and



(c) determining the presence of the compound bound to the DP178 peptide, thereby identifying an agent to be tested for antiviral ability.

5 One method utilizing these types of approaches that may be pursued in the isolation of such DP107-binding or DP178-binding compounds is an assay which would include the attachment of either the DP107 or the DP178 peptide to a solid matrix, such as, for example, agarose or plastic beads, microtiter plate  
10 wells, petri dishes, or membranes composed of, for example, nylon or nitrocellulose. In such an assay system, either the DP107 or DP178 protein may be anchored onto a solid surface, and the compound, or test substance, which is not anchored, is labeled,  
15 either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored component may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface  
20 with a solution of the protein and drying.

Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and  
25 stored.

In order to conduct the assay, the labeled compound is added to the coated surface containing the anchored DP107 or DP178 peptide. After the reaction is complete, unreacted components are removed (e.g.,  
30 by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the compound is pre-labeled, the detection of  
35 label immobilized on the surface indicates that



complexes were formed. Where the labeled component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the compound (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody).

Alternatively, such an assay can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for DP107 or DP178, whichever is appropriate for the given assay, or an antibody specific for the compound, i.e., the test substance, in order to anchor any complexes formed in solution, and a labeled antibody specific for the other member of the complex to detect anchored complexes.

By utilizing procedures such as this, large numbers of types of molecules may be simultaneously screened for DP107 or DP178-binding capability, and thus potential antiviral activity.

Further, compounds may be screened for an ability to inhibit the formation of or, alternatively, disrupt DP107/DP178 complexes. Such compounds may then be tested for antifusogenic, antiviral or intercellular modulatory capability. For ease of description, DP107 and DP178 will be referred to as "binding partners." Compounds that disrupt such interactions may exhibit antiviral activity. Such compounds may include, but are not limited to molecules such as antibodies, peptides, and the like described above.

The basic principle of the assay systems used to identify compounds that interfere with the interaction between the DP107 and DP178 peptides involves preparing a reaction mixture containing peptides under conditions and for a time sufficient to allow the two peptides to interact and bind, thus forming a complex.



In order to test a compound for disruptive activity, the reaction is conducted in the presence and absence of the test compound, i.e., the test compound may be initially included in the reaction mixture, or added at a time subsequent to the addition of one of the binding partners; controls are incubated without the test compound or with a placebo. The formation of any complexes between the binding partners is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound indicates that the compound interferes with the interaction of the DP107 and DP178 peptides.

The assay for compounds that interfere with the interaction of the binding partners can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring one of the binding partners onto a solid phase and detecting complexes anchored on the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance; i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the binding partners. On the other hand, test compounds that disrupt preformed complexes, e.g. compounds with higher binding constants that displace one of the binding partners from the complex, can be tested by adding the test compound to the reaction mixture after complexes have

35



been formed. The various formats are described briefly below.

5 In a heterogeneous assay system, one binding partner, e.g., either the DP107 or DP178 peptide, is anchored onto a solid surface, and its binding partner, which is not anchored, is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored species may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be  
10 accomplished simply by coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

15 In order to conduct the assay, the binding partner of the immobilized species is added to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes  
20 formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the binding partner was pre-labeled, the detection of label immobilized on the surface  
25 indicates that complexes were formed. Where the binding partner is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the binding partner (the antibody, in turn, may be  
30 directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

35



Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one binding partner to anchor any complexes formed in solution, and a labeled antibody specific for the other binding partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds which inhibit complex or which disrupt preformed complexes can be identified.

In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the DP107 and DP178 peptides is prepared in which one of the binding partners is labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the binding partners from the preformed complex will result in the generation of a signal above background. In this way, test substances which disrupt DP-107/DP-178 protein-protein interaction can be identified.

In an alternative screening assay, test compounds may be assayed for the their ability to disrupt a DP178/DP107 interaction, as measured immunometrically using an antibody specifically reactive to a DP107/DP178 complex (i.e., an antibody that recognizes neither DP107 nor DP178 individually). Such an assay acts as a competition assay, and is based on techniques well known to those of skill in the art.

The above competition assay may be described, by way of example, and not by way of limitation, by using the DP178 and M41Δ178 peptides and by assaying test



compounds for the disruption of the complexes formed by these two peptides by immunometrically visualizing DP178/M41Δ178 complexes via the human recombinant Fab, Fab-d, as described, below, in the Example presented in Section 8. M41Δ178 is a maltose binding fusion  
5 protein containing a gp41 region having its DP178 domain deleted, and is described, below, in the Example presented in Section 8.

Utilizing such an assay, M41Δ178 may be immobilized onto solid supports such as microtiter  
10 wells. A series of dilutions of a test compound may then be added to each M41Δ178-containing well in the presence of a constant concentration of DP-178 peptide. After incubation, at, for example, room temperature for one hour, unbound DP-178 and test  
15 compound are removed from the wells and wells are then incubated with the DP178/M41Δ178-specific Fab-d antibody. After incubation and washing, unbound Fab-d is removed from the plates and bound Fab-d is quantitated. A no-inhibitor control should also be  
20 conducted. Test compounds showing an ability to disrupt DP178/M41Δ178 complex formation are identified by their concentration-dependent decrease in the level of Fab-d binding.

A variation of such an assay may be utilized to  
25 perform a rapid, high-throughput binding assay which is capable of directly measuring DP178 binding to M41Δ178 for the determination of binding constants of the ligand or inhibitory constants for competitors of DP178 binding.

30 Such an assay takes advantage of accepted radioligand and receptor binding principles. (See, for example, Yamamura, H.I. et al., 1985, "Neurotransmitter Receptor Binding", 2nd ed., Raven Press, NY.) As above, M41Δ178 is immobilized onto a  
35 solid support such as a microtiter well. DP178



binding to M41Δ178 is then quantitated by measuring the fraction of DP178 that is bound as <sup>125</sup>I-DP178 and calculating the total amount bound using a value for specific activity (dpm/μg peptide) determined for each labeled DP178 preparation. Specific binding to  
5 M41Δ178 is defined as the difference of the binding of the labeled DP178 preparation in the microtiter wells (totals) and the binding in identical wells containing, in addition, excess unlabeled DP178 (nonspecifics).

10

#### 5.5 PHARMACEUTICAL FORMULATIONS, DOSAGES AND MODES OF ADMINISTRATION

The peptides of the invention may be administered using techniques well known to those in the art.  
15 Preferably, agents are formulated and administered systemically. Techniques for formulation and administration may be found in "Remington's Pharmaceutical Sciences", 18th ed., 1990, Mack Publishing Co., Easton, PA. Suitable routes may  
20 include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as, intrathecal, direct intraventricular, intravenous, intraperitoneal,  
25 intranasal, or intraocular injections, just to name a few. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiological saline  
30 buffer. For such transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

In instances wherein intracellular administration  
35 of the peptides of the invention or other inhibitory



agents is preferred, techniques well known to those of ordinary skill in the art may be utilized. For example, such agents may be encapsulated into liposomes, then administered as described above.

5 Liposomes are spherical lipid bilayers with aqueous interiors. All molecules present in an aqueous solution at the time of liposome formation are incorporated into the aqueous interior. The liposomal contents are both protected from the external  
10 microenvironment and, because liposomes fuse with cell membranes, are effectively delivered into the cell cytoplasm. Additionally, due to their hydrophobicity, when small molecules are to be administered, direct intracellular administration may be achieved.

15 Nucleotide sequences encoding the peptides of the invention which are to be intracellularly administered may be expressed in cells of interest, using techniques well known to those of skill in the art. For example, expression vectors derived from viruses such as retroviruses, vaccinia viruses, adeno-  
20 associated viruses, herpes viruses, or bovine papilloma viruses, may be used for delivery and expression of such nucleotide sequences into the targeted cell population. Methods for the construction of such vectors and expression constructs  
25 are well known. See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor NY, and Ausubel et al., 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley  
30 Interscience, NY.

With respect to HIV, peptides of the invention, particularly DP107 and DP178, may be used as  
therapeutics in the treatment of AIDS. In addition,  
35 the peptides may be used as prophylactic measures in previously uninfected individuals after acute exposure



to an HIV virus. Examples of such prophylactic use of the peptides may include, but are not limited to, prevention of virus transmission from mother to infant and other settings where the likelihood of HIV transmission exists, such as, for example, accidents  
5 in health care settings wherein workers are exposed to HIV-containing blood products. The successful use of such treatments do not rely upon the generation of a host immune response directed against such peptides.

Effective dosages of the peptides of the  
10 invention to be administered may be determined through procedures well known to those in the art which address such parameters as biological half-life, bioavailability, and toxicity. Given the data presented below in Section 6, DP178, for example, may  
15 prove efficacious in vivo at doses required to achieve circulating levels of about 1 to about 10 ng per ml of peptide.

A therapeutically effective dose refers to that amount of the compound sufficient to result in  
20 amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD<sub>50</sub>  
25 (the dose lethal to 50% of the population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD<sub>50</sub>/ED<sub>50</sub>. Compounds  
30 which exhibit large therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of  
35 circulating concentrations that include the ED<sub>50</sub> with



little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated  
5 initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the  $IC_{50}$  (e.g., the concentration of the test compound which achieves a half-maximal inhibition of the fusogenic  
10 event, such as a half-maximal inhibition of viral infection relative to the amount of the event in the absence of the test compound) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels  
15 in plasma may be measured, for example, by high performance liquid chromatography (HPLC).

The peptides of the invention may, further, serve the role of a prophylactic vaccine, wherein the host raises antibodies against the peptides of the  
20 invention, which then serve to neutralize HIV viruses by, for example, inhibiting further HIV infection.

Administration of the peptides of the invention as a prophylactic vaccine, therefore, would comprise administering to a host a concentration of peptides  
25 effective in raising an immune response which is sufficient to neutralize HIV, by, for example, inhibiting HIV ability to infect cells. The exact concentration will depend upon the specific peptide to be administered, but may be determined by using  
30 standard techniques for assaying the development of an immune response which are well known to those of ordinary skill in the art. The peptides to be used as vaccines are usually administered intramuscularly.

The peptides may be formulated with a suitable  
35 adjuvant in order to enhance the immunological



response. Such adjuvants may include, but are not limited to mineral gels such as aluminum hydroxide; surface active substances such as lysolecithin, pluronic polyols, polyanions; other peptides; oil emulsions; and potentially useful human adjuvants such as BCG and *Corynebacterium parvum*. Many methods may be used to introduce the vaccine formulations described here. These methods include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, and intranasal routes.

Alternatively, an effective concentration of polyclonal or monoclonal antibodies raised against the peptides of the invention may be administered to a host so that no uninfected cells become infected by HIV. The exact concentration of such antibodies will vary according to each specific antibody preparation, but may be determined using standard techniques well known to those of ordinary skill in the art. Administration of the antibodies may be accomplished using a variety of techniques, including, but not limited to those described in this section.

For all such treatments described above, the exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g. Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p1).

It should be noted that the attending physician would know how to and when to terminate, interrupt, or adjust administration due to toxicity, or to organ dysfunctions. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administered dose in the management of the oncogenic disorder of interest



will vary with the severity of the condition to be treated and the route of administration. The dose and perhaps dose frequency, will also vary according to the age, body weight, and response of the individual patient. A program comparable to that discussed above  
5 may be used in veterinary medicine.

Use of pharmaceutically acceptable carriers to formulate the compounds herein disclosed for the practice of the invention into dosages suitable for systemic administration is within the scope of the  
10 invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular, those formulated as solutions, may be administered parenterally, such as by intravenous injection. The compounds can be  
15 formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups,  
20 slurries, suspensions and the like, for oral ingestion by a patient to be treated.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective  
25 amount to achieve its intended purpose. Determination of the effective amounts is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

In addition to the active ingredients, these  
30 pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated  
35



for oral administration may be in the form of tablets, dragees, capsules, or solutions.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

Pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be



added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

25 6. EXAMPLE: DP178 (SEQ ID:1) IS A POTENT INHIBITOR OF HIV-1 INFECTION

In this example, DP178 (SEQ ID:1) is shown to be a potent inhibitor of HIV-1 mediated CD-4<sup>+</sup> cell-cell fusion and infection by cell free virus. In the fusion assay, this peptide completely blocks virus induced syncytia formation at concentrations of from 1-10 ng/ml. In the infectivity assay the inhibitory concentration is somewhat higher, blocking infection at 90ng/ml. It is further shown that DP178 (SEQ ID:1) shows that the antiviral activity of DP178 (SEQ ID:1)



is highly specific for HIV-1. Additionally, a synthetic peptide, DP-185 (SEQ ID:3), representing a HIV-1-derived DP178 homolog is also found to block HIV-1-mediated syncytia formation.

5

## 6.1. MATERIALS AND METHODS

### 6.1.1. PEPTIDE SYNTHESIS

Peptides were synthesized using Fast Moc chemistry on an Applied Biosystems Model 431A peptide synthesizer. Generally, unless otherwise noted, the peptides contained amidated carboxy termini and acetylated amino termini. Amidated peptides were prepared using Rink resin (Advanced Chemtech) while peptides containing free carboxy termini were synthesized on Wang (p-alkoxy-benzyl-alcohol) resin (Bachem). First residues were double coupled to the appropriate resin and subsequent residues were single coupled. Each coupling step was followed by acetic anhydride capping. Peptides were cleaved from the resin by treatment with trifluoroacetic acid (TFA) (10ml), H<sub>2</sub>O (0.5ml), thioanisole (0.5ml), ethanedithiol (0.25ml), and crystalline phenol (0.75g). Purification was carried out by reverse phase HPLC. Approximately 50mg samples of crude peptide were chromatographed on a Waters Delta Pak C18 column (19mm x 30cm, 15 $\mu$  spherical) with a linear gradient; H<sub>2</sub>O/acetonitrile 0.1% TFA. Lyophilized peptides were stored desiccated and peptide solutions were made in water at about 1mg/ml. Electrospray mass spectrometry yielded the following results: DP178 (SEQ ID:1):4491.87 (calculated 4491.94); DP-180 (SEQ ID:2):4491.45 (calculated 4491.94); DP-185 (SEQ ID:3):not done (calculated 4546.97).

35



6.1.2. VIRUS

The HIV-1<sub>LAI</sub> virus was obtained from R. Gallo (Popovic, M. et al., 1984, Science 224:497-508) and propagated in CEM cells cultured in RPMI 1640  
5 containing 10% fetal calf serum. Supernatant from the infected CEM cells was passed through a 0.2 $\mu$ m filter and the infectious titer estimated in a microinfectivity assay using the AA5 cell line to support virus replication. For this purpose, 25 $\mu$ l of  
10 serial diluted virus was added to 75 $\mu$ l AA5 cells at a concentration of  $2 \times 10^5$ /ml in a 96-well microtitre plate. Each virus dilution was tested in triplicate. Cells were cultured for eight days by addition of fresh medium every other day. On day 8 post  
15 infection, supernatant samples were tested for virus replication as evidenced by reverse transcriptase activity released to the supernatant. The TCID<sub>50</sub> was calculated according to the Reed and Muench formula (Reed, L.J. et al., 1938, Am. J. Hyg. 27:493-497).  
20 The titer of the HIV-1<sub>LAI</sub> and HIV-1<sub>MN</sub> stocks used for these studies, as measured on the AA5 cell line, was approximately  $1.4 \times 10^6$  and  $3.8 \times 10^4$  TCID<sub>50</sub>/ml, respectively.

6.1.3. CELL FUSION ASSAY

25 Approximately  $7 \times 10^4$  Molt cells were incubated with  $1 \times 10^4$  CEM cells chronically infected with the HIV-1<sub>LAI</sub> virus in 96-well plates (one-half area cluster plates; Costar, Cambridge, MA) in a final volume of 100 $\mu$ l culture medium as previously described  
30 (Matthews, T.J. et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5428). Peptide inhibitors were added in a volume of 10 $\mu$ l and the cell mixtures were incubated for 24 hr. at 37°C. At that time, multinucleated  
35 giant cells were estimated by microscopic examination



at a 40x magnification which allowed visualization of the entire well in a single field.

#### 6.1.4. CELL FREE VIRUS INFECTION ASSAY

Synthetic peptides were incubated at 37°C with  
5 either 247 TCID<sub>50</sub> (for experiment depicted in FIG. 2),  
or 62 TCID<sub>50</sub> (for experiment depicted in FIG.3) units  
of HIV-1<sub>LAI</sub> virus or 25 TCID<sub>50</sub> units of HIV-2<sub>NIH</sub> and CEM  
CD4<sup>+</sup> cells at peptide concentrations of 0, 0.04, 0.4,  
4.0, and 40µg/ml for 7 days. The resulting reverse  
10 transcriptase (RT) activity in counts per minute was  
determined using the assay described, below, in  
Section 6.1.5. See, Reed, L.J. et al., 1938, Am. J.  
Hyg. 27: 493-497 for an explanation of TCID<sub>50</sub>  
calculations.

#### 6.1.5. REVERSE TRANSCRIPTASE ASSAY

The micro-reverse transcriptase (RT) assay was  
adapted from Goff et al. (Goff, S. et al., 1981, J.  
Virol. 38:239-248) and Willey et al. (Willey, R. et  
20 al., 1988, J. Virol. 62:139-147). Supernatants from  
virus/cell cultures are adjusted to 1% Triton-X100. A  
10µl sample of supernatant was added to 50µl of RT  
cocktail in a 96-well U-bottom microtitre plate and  
the samples incubated at 37°C for 90 min. The RT  
25 cocktail contained 75mM KCl, 2mM dithiothreitol, 5mM  
MgCl<sub>2</sub>, 5µg/ml poly A (Pharmacia, cat. No. 27-4110-01),  
0.25 units/ml oligo dT (Pharmacia, cat. No. 27-7858-  
01), 0.05% NP40, 50mM Tris-HCl, pH 7.8, 0.5µM non-  
radioactive dTTP, and 10µCi/ml <sup>32</sup>P-dTTP (Amersham, cat.  
30 No. PB.10167).

After the incubation period, 40µl of reaction  
mixture was applied to a Schleicher and Schuell (S+S)  
NA45 membrane (or DE81 paper) saturated in 2 x SSC  
buffer (0.3M NaCl and 0.003M sodium citrate) held in a  
35 S+S Minifold over one sheet of GB003 (S+S) filter







paper, with partial vacuum applied. Each well of the minifold was washed four times with 200 $\mu$ l 2xSSC, under full vacuum. The membrane was removed from the minifold and washed 2 more times in a pyrex dish with an excess of 2xSSC. Finally, the membrane was drained  
5 on absorbent paper, placed on Whatman #3 paper, covered with Saran wrap, and exposed to film overnight at -70°C.

## 6.2. RESULTS

### 10 6.2.1. PEPTIDE INHIBITION OF INFECTED CELL-INDUCED SYNCYTIA FORMATION

The initial screen for antiviral activity assayed peptides' ability to block syncytium formation induced by overnight co-cultivation of uninfected Molt4 cells  
15 with chronically HIV-1 infected CEM cells. The results of several such experiments are presented herein. In the first of these experiments, serial DP178 (SEQ ID:1) peptide concentrations between 10 $\mu$ g/ml and 12.5ng/ml were tested for blockade of the  
20 cell fusion process. For these experiments, CEM cells chronically infected with either HIV-1<sub>LAI</sub>, HIV-1<sub>MN</sub>, HIV-1<sub>RF</sub>, or HIV-1<sub>SF2</sub> virus were cocultivated overnight with uninfected Molt 4 cells. The results (FIG. 4) show that DP178 (SEQ ID:1) afforded complete protection  
25 against each of the HIV-1 isolates down to the lowest concentration of DP178 (SEQ ID:1) used. For HIV<sub>LAI</sub> inhibition, the lowest concentration tested was 12.5ng/ml; for all other HIV-1 viruses, the lowest concentration of DP178 (SEQ ID:1) used in this study  
30 was 100ng/ml. A second peptide, DP-180 (SEQ ID:2), containing the same amino acid residues as DP178 (SEQ ID:1) but arranged in a random order exhibited no evidence of anti-fusogenic activity even at the high concentration of 40 $\mu$ g/ml (FIG. 4). These observations  
35 indicate that the inhibitory effect of DP178 (SEQ



ID:1) is primary sequence-specific and not related to non-specific peptide/protein interactions. The actual endpoint (i.e., the lowest effective inhibitory concentration) of DP178 inhibitory action is within the range of 1-10 ng/ml.

5       The next series of experiments involved the preparation and testing of a DP178 (SEQ ID:1) homolog for its ability to inhibit HIV-1-induced syncytia formation. As shown in FIG. 1, the sequence of DP-185 (SEQ ID:3) is slightly different from DP178 (SEQ ID:1) in that its primary sequence is taken from the HIV-1<sub>SR2</sub> isolate and contains several amino acid differences relative to DP178 (SEQ ID:1) near the N terminus. As shown in FIG. 4, DP-185 (SEQ ID:3), exhibits inhibitory activity even at 312.5ng/ml, the lowest concentration tested.

10       The next series of experiments involved a comparison of DP178 (SEQ ID:1) HIV-1 and HIV-2 inhibitory activity. As shown in FIG. 5, DP178 (SEQ ID:1) blocked HIV-1-mediated syncytia formation at peptide concentrations below 1ng/ml. DP178 (SEQ ID:1) failed, however, to block HIV-2 mediated syncytia formation at concentrations as high as 10µg/ml. This striking 4 log selectivity of DP178 (SEQ ID:1) as an inhibitor of HIV-1-mediated cell fusion demonstrates an unexpected HIV-1 specificity in the action of DP178 (SEQ ID:1). DP178 (SEQ ID:1) inhibition of HIV-1-mediated cell fusion, but the peptide's inability to inhibit HIV-2 mediated cell fusion in the same cell type at the concentrations tested provides further evidence for the high degree of selectivity associated with the antiviral action of DP178 (SEQ ID:1).

35



### 6.2.2. PEPTIDE INHIBITION OF INFECTION BY CELL-FREE VIRUS

DP178 (SEQ ID:1) was next tested for its ability to block CD-4<sup>+</sup> CEM cell infection by cell free HIV-1 virus. The results, shown in FIG. 2, are from an experiment in which DP178 (SEQ ID:1) was assayed for its ability to block infection of CEM cells by an HIV-1<sub>LAI</sub> isolate. Included in the experiment were three control peptides, DP-116 (SEQ ID:9), DP-125 (SEQ ID:8), and DP-118 (SEQ ID:10). DP-116 (SEQ ID:9) represents a peptide previously shown to be inactive using this assay, and DP-125 (SEQ ID:8; Wild, C. et al., 1992, Proc. Natl. Acad. Sci. USA 89:10,537) and DP-118 (SEQ ID:10) are peptides which have previously been shown to be active in this assay. Each concentration (0, 0.04, 0.4, 4, and 40 $\mu$ g/ml) of peptide was incubated with 247 TCID<sub>50</sub> units of HIV-1<sub>LAI</sub> virus and CEM cells. After 7 days of culture, cell-free supernatant was tested for the presence of RT activity as a measure of successful infection. The results, shown in FIG. 2, demonstrate that DP178 (SEQ ID:1) inhibited the de novo infection process mediated by the HIV-1 viral isolate at concentrations as low as 90ng/ml (IC<sub>50</sub>=90ng/ml). In contrast, the two positive control peptides, DP-125 (SEQ ID:8) and DP-118 (SEQ ID:10), had over 60-fold higher IC<sub>50</sub> concentrations of approximately 5 $\mu$ g/ml.

In a separate experiment, the HIV-1 and HIV-2 inhibitory action of DP178 (SEQ ID:1) was tested with CEM cells and either HIV-1<sub>LAI</sub> or HIV-2<sub>NIH2</sub>. 62 TCID<sub>50</sub> HIV-1<sub>LAI</sub> or 25 GCID<sub>50</sub> HIV-2<sub>NIH2</sub> were used in these experiments, and were incubated for 7 days. As may be seen in FIG. 3, DP178 (SEQ ID:1) inhibited HIV-1 infection with an IC<sub>50</sub> of about 31ng/ml. In contrast, DP178 (SEQ ID:1) exhibited a much higher IC<sub>50</sub> for HIV-2<sub>NIH2</sub>, thus making DP178 (SEQ ID:1) two logs more potent



as a HIV-1 inhibitor than a HIV-2 inhibitor. This finding is consistent with the results of the fusion inhibition assays described, above, in Section 6.2.1, and further supports a significant level of selectivity (i.e., for HIV-1 over HIV-2).

5

7. EXAMPLE: THE HIV-1 INHIBITOR, DP178 (SEQ ID:1) IS NON-CYTOTOXIC

In this Example, the 36 amino acid synthetic peptide inhibitor DP178 (SEQ ID:1) is shown to be non-  
10 cytotoxic to cells in culture, even at the highest peptide concentrations (40µg/ml) tested.

7.1. MATERIALS AND METHODS

Cell proliferation and toxicity assay:

15 Approximately  $3.8 \times 10^5$  CEM cells for each peptide concentration were incubated for 3 days at 37°C in T25 flasks. Peptides tested were DP178 (SEQ ID:1) and DP-116 (SEQ ID:9), as described in FIG. 1. Peptides were synthesized as described, above, in Section 6.1. The  
20 concentrations of each peptide used were 0, 2.5, 10, and 40µg/ml. Cell counts were taken at incubation times of 0, 24, 48, and 72 hours.

7.2. RESULTS

25 Whether the potent HIV-1 inhibitor DP178 (SEQ ID:1) exhibited any cytotoxic effects was assessed by assaying the peptide's effects on the proliferation and viability of cells in culture. CEM cells were incubated in the presence of varying concentrations of  
30 DP178 (SEQ ID:1), and DP-116 (SEQ ID:9), a peptide previously shown to be ineffective as a HIV inhibitor (Wild, C. et al., 1992, Proc. Natl. Acad. Sci. USA 89:10,537-10,541). Additionally, cells were incubated in the absence of either peptide.

35



The results of the cytotoxicity study demonstrate that DP178 (SEQ ID:1) exhibits no cytotoxic effects on cells in culture. As can be seen, below, in Table XXIV, even the proliferation and viability characteristics of cells cultured for 3 days in the presence of the highest concentration of DP178 (SEQ ID:1) tested (40 $\mu$ g/ml) do not significantly differ from the DP-116 (SEQ ID:9) or the no-peptide controls. The cell proliferation data is also represented in graphic form in FIG. 6. As was demonstrated in the Working Example presented above in Section 6, DP178 (SEQ ID:1) completely inhibits HIV-1 mediated syncytia formation at peptide concentrations between 1 and 10ng/ml, and completely inhibits cell-free viral infection at concentrations of at least 90ng/ml. Thus, this study demonstrates that even at peptide concentrations greater than 3 log higher than the HIV inhibitory dose, DP178 (SEQ ID:1) exhibits no cytotoxic effects.



TABLE XXIV

5	Peptide	Peptide Concentration $\mu\text{g/ml}$	% Viability at time (hours)			
			0	24	48	72
10	DP178 (SEQ ID:1)	40	98	97	95	97
		10	98	97	98	98
		2.5	98	93	96	96
15	DP116 (SEQ ID:9)	40	98	95	98	97
		10	98	95	93	98
		2.5	98	96	98	99
20	No Peptide	0	98	97	99	98

8. EXAMPLE: THE INTERACTION OF DP178 AND DP107

Soluble recombinant forms of gp41 used in the  
 25 example described below provide evidence that the  
 DP178 peptide associates with a distal site on gp41  
 whose interactive structure is influenced by the DP107  
 leucine zipper motif. A single mutation disrupting  
 the coiled-coil structure of the leucine zipper domain  
 30 transformed the soluble recombinant gp41 protein from  
 an inactive to an active inhibitor of HIV-1 fusion.  
 This transformation may result from liberation of the  
 potent DP178 domain from a molecular clasp with the  
 leucine zipper, DP107, determinant. The results also  
 35 indicate that the anti-HIV activity of various gp41  
 derivatives (peptides and recombinant proteins) may be



due to their ability to form complexes with viral gp41 and interfere with its fusogenic process.

## 8.1. MATERIALS AND METHODS

### 5                   8.1.1. CONSTRUCTION OF FUSION PROTEINS                   AND GP41 MUTANTS

Construction of fusion proteins and mutants shown in FIG. 7 was accomplished as follows: the DNA sequence corresponding to the extracellular domain of gp41 (540-686) was cloned into the Xmn I site of the expression vector pMal-p2 (New England Biolab) to give M41. The gp41 sequence was amplified from pgtat (Malim et al., 1988, Nature 355: 181-183) by using polymerase chain reaction (PCR) with upstream primer 10 5'-ATGACGCTGACGGTACAGGCC-3' (primer A) and downstream primer 5'-TGACTAAGCTTAATACCACAGCCAATTTGTTAT-3' (primer B). M41-P was constructed by using the T7-Gen in vitro mutagenesis kit from United States Biochemicals (USB) following the supplier's 20 instructions. The mutagenic primer (5'-GGAGCTGCTTGGGGCCCCAGAC-3') introduces an Ile to Pro mutation in M41 at position 578. M41Δ107, from which the DP-107 region has been deleted, was made using a deletion mutagenic primer 5'- 25 CCAAATCCCCAGGAGCTGCTCGAGCTGCACTATACCAGAC-3' (primer C) following the USB T7-Gen mutagenesis protocol. M41Δ178, from which the DP-178 region has been deleted, was made by cloning the DNA fragment corresponding to gp41 amino acids 540-642 into the 30 Xmn I site of pMal-p2. Primer A and 5'-ATAGCTTCTAGATTAATTGTTAATTTCTCTGTCCC-3' (primer D) were used in the PCR with the template pgtat to generate the inserted DNA fragments. M41-P was used as the template with primer A and D in PCR to generate M41- 35 PA178. All inserted sequences and mutated residues



were checked by restriction enzyme analysis and confirmed by DNA sequencing.

#### 8.1.2. PURIFICATION AND CHARACTERIZATION OF FUSION PROTEINS

5       The fusion proteins were purified according to the protocol described in the manufacturer's brochure of protein fusion and purification systems from New England Biolabs (NEB). Fusion proteins (10 ng) were analyzed by electrophoresis on 8% SDS polyacrylamide  
10       gels. Western blotting analysis was performed as described by Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2d Ed, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, Ch. 18, pp. 64-75. An HIV-1 positive serum diluted 1000-fold,  
15       or a human Fab derived from repertoire cloning was used to react with the fusion proteins. The second antibody was HRP-conjugated goat antihuman Fab. An ECL Western blotting detection system (Amersham) was used to detect the bound antibody. A detailed  
20       protocol for this detection system was provided by the manufacturer. Rainbow molecular weight markers (Amersham) were used to estimate the size of fusion proteins.

#### 25       8.1.3. CELL FUSION ASSAYS FOR ANTI-HIV ACTIVITY

Cell fusion assays were performed as previously described (Matthews et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5481). CEM cells ( $7 \times 10^4$ ) were incubated with HIV-1<sub>ms</sub> chronically infected CEM cells  
30       ( $10^4$ ) in 96-well flat-bottomed half-area plates (Costar) in 100  $\mu$ l culture medium. Peptide and fusion proteins at various concentrations in 10  $\mu$ l culture medium were incubated with the cell mixtures at 37°C for 24 hours. Multinucleated syncytia were estimated  
35       with microscopic examination. Both M41 and M41-P did



not show cytotoxicity at the concentrations tested and shown in FIG. 8.

Inhibition of HIV-1 induced cell-cell fusion activity was carried out in the presence of 10 nM DP178 and various concentrations of M41Δ178 or M41-PA178 as indicated in FIG. 9. There was no observable syncytia in the presence of 10 nM DP178. No peptide or fusion protein was added in the control samples.

8.1.4. ELISA ANALYSIS OF DP178 BINDING TO THE LEUCINE ZIPPER MOTIF OF GP41

The amino acid sequence of DP178 used is: YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF. For enzyme linked immunoassay (ELISA), M41Δ178 or M41-PA178 (5 μg/ml) in 0.1M NaHCO<sub>3</sub>, pH 8.6, were coated on 96 wells Linbro ELISA plates (Flow Lab, Inc.) overnight. Each well was washed three times with distilled water then blocked with 3% bovine serum albumin (BSA) for 2 hours. After blocking, peptides with 0.5% BSA in TBST (40 mM Tris-HCl pH7.5, 150 mM NaCl, 0.05% Tween 20) were added to the ELISA plates and incubated at room temperature for 1 hour. After washing three times with TBST, Fab-d was added at a concentration of 10 ng/ml with 0.5% BSA in TBST. The plates were washed three times with TBST after incubation at room temperature for 1 hour. Horse radish peroxidase (HRP) conjugated goat antihuman Fab antiserum at a 2000 fold dilution in TBST with 0.5% BSA was added to each well and incubated at room temperature for 45 minutes. The plates were then washed four times with TBST. The peroxidase substrate o-phenylene diamine (2.5 mg/ml) and 0.15% H<sub>2</sub>O<sub>2</sub> were added to develop the color. The reaction was stopped with an equal volume of 4.5 N H<sub>2</sub>SO<sub>4</sub> after incubation at room temperature for 10 minutes. The optical density of the stopped reaction mixture was measured with a micro plate reader



(Molecular Design) at 490 nm. Results are shown in FIG. 10.

## 8.2. RESULTS

### 5 8.2.1. THE EXPRESSION AND CHARACTERIZATION OF THE ECTODOMAIN OF gp41

As a step toward understanding the roles of the two helical regions in gp41 structure and function, the ectodomain of gp41 was expressed as a maltose binding fusion protein (M41) (FIG. 7). The fusogenic  
10 peptide sequence at the N-terminal of gp41 was omitted from this recombinant protein and its derivatives to improve solubility. The maltose binding protein facilitated purification of the fusion proteins under relatively mild, non-denaturing conditions. Because  
15 the M41 soluble recombinant gp41 was not glycosylated, lacked several regions of the transmembrane protein (*i.e.*, the fusion peptide, the membrane spanning, and the cytoplasmic domains), and was expressed in the absence of gp120, it was not expected to precisely  
20 reflect the structure of native gp41 on HIV-1 virions. Nevertheless, purified M41 folded in a manner that preserved certain discontinuous epitopes as evidenced by reactivity with human monoclonal antibodies, 98-6, 126-6, and 50-69, previously shown to bind  
25 conformational epitopes on native gp41 expressed in eukaryotic cells (Xu et al., 1991, J. Virol. 65: 4832-4838; Chen, 1994, J. Virol. 68:2002-2010). Thus, at least certain regions of native gp41 defined by these antibodies appear to be reproduced in the recombinant  
30 fusion protein M41. Furthermore, M41 reacted with a human recombinant Fab (Fab-d) that recognizes a conformational epitope on gp41 and binds HIV-1 virions as well as HIV-1 infected cells but not uninfected cells as analyzed by FACS. Deletion of either helix  
35 motif, *i.e.*, DP107 or DP178, of the M41 fusion protein



eliminated reactivity with Fab-d. These results indicate that both helical regions, separated by 60 amino acids in the primary sequence, are required to maintain the Fab-d epitope.

5

#### 8.2.2. ANTI-HIV ACTIVITY OF THE RECOMBINANT ECTODOMAIN OF GP41

The wild type M41 fusion protein was tested for anti-HIV-1 activity. As explained, *supra*, synthetic peptides corresponding to the leucine zipper (DP107) and the C-terminal putative helix (DP178) show potent anti-HIV activity. Despite inclusion of both these regions, the recombinant M41 protein did not affect HIV-1 induced membrane fusion at concentrations as high as 50  $\mu$ M (Table XXV, below).

---

**TABLE XXV**

**DISRUPTION OF THE LEUCINE ZIPPER OF  
GP41 FREES THE ANTI-HIV MOTIF**

	<u>DP107</u>	<u>DP178</u>	<u>M41</u>	<u>M41-P</u>	<u>M41-PA178</u>
Cell fusion (IC <sub>50</sub> )	1 $\mu$ M	1 nM	> 50 $\mu$ M	83 nM	> 50 $\mu$ M
Fab-D binding (K <sub>D</sub> )	-	-	3.5x10 <sup>-9</sup>	2.5x10 <sup>-8</sup>	-
HIV infectiv- ity (IC <sub>50</sub> )	1 $\mu$ M	80 nM	> 16 $\mu$ M	66 nM	> 8 $\mu$ M

The affinity constants of Fab-d binding to the fusion proteins were determined using a protocol described by B. Friguet et al., 1985, J. Immunol. Method. 77:305-319.

- = No detectable binding of Fab-d to the fusion proteins.

*Antiviral Infectivity Assays.* 20  $\mu$ l of serially diluted virus stock was incubated for 60 minutes at ambient temperature with 20  $\mu$ l of the indicated



concentration of purified recombinant fusion protein in RPMI 1640 containing 10% fetal bovine serum and antibiotics in a 96-well microtiter plate. 20  $\mu$ l of CEM4 cells at  $6 \times 10^5$  cells/ml were added to each well, and cultures were incubated at 37°C in a humidified CO<sub>2</sub> incubator. Cells were cultured for 9 days by the addition of fresh medium every 2 to 3 days. On days 5, 7, and 9 postinfection, supernatant samples were assayed for reverse transcriptase (RT) activity, as described below, to monitor viral replication. The 50% tissue culture infectious dose (TCID<sub>50</sub>) was calculated for each condition according to the formula of Reed & Muench, 1937, Am. J. Hyg. 27:493-497. RT activity was determined by a modification of the published methods of Goff et al., 1981, J. Virol. 38:239-248 and Willey et al., 1988, J. Virol. 62:139-147 as described in Chen et al., 1993, AIDS Res. Human Retroviruses 9:1079-1086.

Surprisingly, a single amino acid substitution, proline in place of isoleucine in the middle of the leucine zipper motif, yielded a fusion protein (M41-P) which did exhibit antiviral activity (Table XXV and Fig. 8). As seen in Table XXV, M41-P blocked syncytia formation by 90% at approximately 85 nM and neutralized HIV-1<sub>MB</sub> infection by 90% at approximately 70 nM concentrations. The anti-HIV-1 activity of M41-P appeared to be mediated by the C-terminal helical sequence since deletion of that region from M41-P yielded an inactive fusion protein, M41-PA178 (Table XXV). This interpretation was reinforced by experiments demonstrating that a truncated fusion protein lacking the DP178 sequence, M41 $\Delta$ 178, abrogated the potent anti-fusion activity of the DP178 peptide in a concentration-dependent manner (FIG. 9). The same truncated fusion protein containing the proline mutation disrupting the leucine zipper, M41-PA178, was not active in similar competition experiments (FIG. 9). The results indicate that the DP178 peptide associates with a second site on gp41 whose interactive structure is dependent on a wild type leucine zipper sequence. A similar interaction may occur within the wild type fusion protein, M41, and act to form an intramolecular clasp which sequesters



the DP178 region, making it unavailable for anti-viral activity.

A specific association between these two domains is also indicated by other human monoclonal Fab-d studies. For example, Fab-d failed to bind either the DP178 peptide or the fusion protein M41Δ178, but its epitope was reconstituted by simply mixing these two reagents together (FIG. 10). Again, the proline mutation in the leucine zipper domain of the fusion protein, M41-PA178, failed to reconstitute the epitope in similar mixing experiments.

9. EXAMPLE: METHOD FOR COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES

A number of known coiled-coil sequences have been well described in the literature and contain heptad repeat positioning for each amino acid. Coiled-coil nomenclature labels each of seven amino acids of a heptad repeat A through G, with amino acids A and D tending to be hydrophobic positions. Amino acids E and G tend to be charged. These four positions (A, D, E, and G) form the amphipathic backbone structure of a monomeric alpha-helix. The backbones of two or more amphipathic helices interact with each other to form di-, tri-, tetrameric, etc., coiled-coil structures. In order to begin to design computer search motifs, a series of well characterized coiled coils were chosen including yeast transcription factor GCN4, Influenza Virus hemagglutinin loop 36, and human proto-oncogenes c-Myc, c-Fos, and c-Jun. For each peptide sequence, a strict homology for the A and D positions, and a list of the amino acids which could be excluded for the B, C, E, F, and G positions (because they are not observed in these positions) was determined. Motifs were tailored to the DP107 and DP178 sequences by



deducing the most likely possibilities for heptad positioning of the amino acids of HIV-1 Bru DP-107, which is known to have coiled-coil structure, and HIV-1 Bru DP178, which is still structurally undefined. The analysis of each of the sequences is contained in FIG. 12. For example, the motif for GCN4 was designed as follows:

1. The only amino acids (using standard single letter amino acid codes) found in the A or D positions of GCN4 were [LMNV].
2. All amino acids were found at B, C, E, F, and G positions except {CFGIMPTW}.
3. The PESEARCH motif would, therefore, be written as follows:

[LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-  
[LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-  
[LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-  
[LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)

Translating or reading the motif: "at the first A position either L, M, N, or V must occur; at positions B and C (the next two positions) accept everything except C, F, G, I, M, P, T, or W; at the D position either L, M, N, or V must occur; at positions E, F, and G (the next 3 positions) accept everything except C, F, G, I, M, P, T, or W." This statement is contained four times in a 28-mer motif and five times in a 35-mer motif. The basic motif key then would be: [LMNV]-{CFGIMPTW}. The motif keys for the remaining well described coiled-coil sequences are summarized in FIG. 12.

The motif design for DP107 and DP178 was slightly different than the 28-mer model sequences described above due to the fact that heptad repeat positions are not defined and the peptides are both longer than 28 residues. FIG. 13 illustrates several possible



sequence alignments for both DP107 and DP178 and also includes motif designs based on 28-mer, 35-mer, and full-length peptides. Notice that only slight differences occur in the motifs as the peptides are lengthened. Generally, lengthening the base peptide results in a less stringent motif. This is very useful in broadening the possibilities for identifying DP107-or DP-178-like primary amino acid sequences referred to in this document as "hits".

In addition to making highly specific motifs for each type peptide sequence to be searched, it is also possible to make "hybrid" motifs. These motifs are made by "crossing" two or more very stringent motifs to make a new search algorithm which will find not only both "parent" motif sequences but also any peptide sequences which have similarities to one, the other, or both "parents". For example, in FIG. 14 the "parent" sequence of GCN4 is crossed with each of the possible "parent" motifs of DP-107. Now the hybrid motif must contain all of the amino acids found in the A and D positions of both parents, and exclude all of the amino acids not found in either parent at the other positions. The resulting hybrid from crossing GCN4 or [LMNV]{CFGIMPTW} and DP107 (28-mer with the first L in the D position) or [ILQT]{CDFIMPST}, is [ILMNQTV]{CFIMPT}. Notice that now only two basic hybrid motifs exist which cover both framing possibilities, as well as all peptide lengths of the parent DP-107 molecule. FIG. 15 represents the "hybridizations" of GCN4 with DP-178. FIG. 16 represents the "hybridizations" of DP107 and DP178. It is important to keep in mind that the represented motifs, both parent and hybrid, are motif keys and not the depiction of the full-length motif needed to actually do the computer search.

35



Hybridizations can be performed on any combination of two or more motifs. FIG. 17 summarizes several three-motif hybridizations including GCN4, DP107 (both frames), and DP178 (also both frames). Notice that the resulting motifs are now becoming much more similar to each other. In fact, the first and third hybrid motifs are actually subsets of the second and fourth hybrid motifs respectively. This means that the first and third hybrid motifs are slightly more stringent than the second and fourth. It should also be noted that with only minor changes in these four motifs, or by hybridizing them, a single motif could be obtained which would find all of the sequences. However, it should be remembered that stringency is also reduced. Finally, the most broad-spectrum and least-stringent hybrid motif is described in FIG. 18 which summarizes the hybridization of GCN4, DP107 (both frames), DP178 (both frames), c-Fos, c-Jun, c-Myc, and Flu loop 36.

A special set of motifs was designed based on the fact that DP-178 is located only approximately ten amino acids upstream of the transmembrane spanning region of gp41 and just C-terminal to a proline which separates DP107 and DP178. It has been postulated that DP178 may be an amphipathic helix when membrane associated, and that the proline might aid in the initiation of the helix formation. The same arrangement was observed in Respiratory Syncytial Virus; however, the DP178-like region in this virus also had a leucine zipper just C-terminal to the proline. Therefore, N-terminal proline-leucine zipper motifs were designed to analyze whether any other viruses might contain this same pattern. The motifs are summarized in FIG. 19.

The PC/Gene protein database contains 5879 viral amino acid sequences (library file PVIRUSES; CD-ROM



release 11.0). Of these, 1092 are viral enveloped or glycoprotein sequences (library file PVIRUSE1). Tables V through XIV contain lists of protein sequence names and motif hit locations for all the motifs searched.

5

10. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION  
OF DP107 AND DP178-LIKE SEQUENCES  
IN HUMAN IMMUNODEFICIENCY VIRUS**

FIG. 20 represents search results for HIV-1 BRU isolate gp41 (PC/Gene protein sequence PENV\_HV1BR). Notice that the hybrid motif which crosses DP-107 and DP-178 (named 107x178x4; the same motif as found in FIG. 16 found three hits including amino acids 550-599, 636-688, and 796-823. These areas include DP-107 plus eight N-terminal and four C-terminal amino acids; DP178 plus seven N-terminal and ten C-terminal amino acids; and an area inside the transmembrane region (cytoplasmic). FIG. 20 also contains the results obtained from searching with the motif named ALLMOTI5, for which the key is found in FIG. 17 ({CDGHP}{CFP}x5). This motif also found three hits including DP107 (amino acids 510-599), DP178 (615-717), and a cytoplasmic region (772-841). These hits overlap the hits found by the motif 107x178x4 with considerable additional sequences on both the amino and carboxy termini. This is not surprising in that 107x178x4 is a subset of the ALLMOTI5 hybrid motif. Importantly, even though the stringency of ALLMOTI5 is considerably less than 107x178x4, it still selectively identifies the DP107 and DP178 regions of gp41 shown to contain sequences for inhibitory peptides of HIV-1. The results of these two motif searches are summarized in Table V under the PC/Gene protein sequence name PENV HV1BR. The proline-leucine zipper motifs also gave several hits in HIV-1 BRU including 503-525 which is



at the very C-terminus of gp120, just upstream of the cleavage site (P7LZIPC and P12LZIPC); and 735-768 in the cytoplasmic domain of gp41 (P23LZIPC). These results are found in Tables VIII, IX, and X under the same sequence name as mentioned above. Notice that the only area of HIV-1 BRU which is predicted by the Lupas algorithm to contain a coiled-coil region, is from amino acids 635-670. This begins eight amino acids N-terminal to the start and ends eight amino acids N-terminal to the end of DP178. DP107, despite the fact that it is a known coiled coil, is not predicted to contain a coiled-coil region using the Lupas method.

11. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN HUMAN RESPIRATORY SYNCYTIAL VIRUS

FIG. 21 represents search results for Human Respiratory Syncytial Virus (RSV; Strain A2) fusion glycoprotein F1 (PC/Gene protein sequence name PVGLF\_HRSVA). Motif 107x178x4 finds three hits including amino acids 152-202, 213-243, and 488-515. The arrangement of these hits is similar to what is found in HIV-1 except that the motif finds two regions with similarities to DP-178, one just downstream of what would be called the DP107 region or amino acids 213-243, and one just upstream of the transmembrane region (also similar to DP178) or amino acids 488-515. Motif ALLMOTI5 also finds three areas including amino acids 116-202, 267-302, and 506-549. The proline-leucine zipper motifs also gave several hits including amino acids 205-221 and 265-287 (P1LZIPC 265-280, P12LZIPC), and 484-513 (P7LZIPC and P12LZIPC 484-506, P23LZIPC). Notice that the PLZIP motifs also identify regions which share location similarities with DP-178 of HIV-1.



12. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP107-LIKE AND DP178-LIKE SEQUENCES  
IN SIMIAN IMMUNODEFICIENCY VIRUS

Motif hits for Simian immunodeficiency Virus gp41 (AGM3 isolate; PC/Gene protein sequence name PENV\_SIVAG) are shown in FIG. 22. Motif 107x178x4 finds three hits including amino acids 566-593, 597-624, and 703-730. The first two hits only have three amino acids between them and could probably be combined into one hit from 566-624 which would represent a DP107-like hit. Amino acids 703 to 730 would then represent a DP178-like hit. ALLMOTI5 also finds three hits including amino acids 556-628 (DP107-like), 651-699 (DP178-like), and 808-852 which represents the transmembrane spanning region. SIV also has one region from 655-692 with a high propensity to form a coiled coil as predicted by the Lupas algorithm. Both 107x178x4 and ALLMOTI5 motifs find the same region. SIV does not have any PLZIP motif hits in gp41.

The identification of DP178/DP107 analogs for a second SIV isolate (MM251) is demonstrated in the Example presented, below, in Section 19.

13. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP107-LIKE AND DP178 LIKE SEQUENCES  
IN CANINE DISTEMPER VIRUS

Canine Distemper Virus (strain Onderstepoort) fusion glycoprotein F1 (PC/Gene Protein sequence name PVGLF\_CDVO) has regions similar to Human RSV which are predicted to be DP107-like and DP178-like (FIG. 23). Motif 107x178x4 highlights one area just C-terminal to the fusion peptide at amino acids 252-293. Amino acids 252-286 are also predicted to be coiled coil using the Lupas algorithm. Almost 100 amino acids C-terminal to the first region is a DP178-like area at residues 340-367. ALLMOTI5 highlights three areas of



interest including: amino acids 228-297, which completely overlaps both the Lupas prediction and the DP107-like 107x178x4 hit; residues 340-381, which overlaps the second 107x178x4 hit; and amino acids 568-602, which is DP178-like in that it is located just N-terminal to the transmembrane region. It also overlaps another region (residues 570-602) predicted by the Lupas method to have a high propensity to form a coiled coil. Several PLZIP motifs successfully identified areas of interest including P6 and P12LZIPC which highlight residues 336-357 and 336-361 respectively; P1 and P12LZIPC which find residues 398-414; and P12 and P23LZIPC which find residues 562-589 and 562-592 respectively.

14. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN NEWCASTLE DISEASE VIRUS

FIG. 24 shows the motif hits found in Newcastle Disease Virus (strain Australia-Victoria/32; PC Gene protein sequence name PVGLF\_NDVA). Motif 107x178x4 finds two areas including a DP107-like hit at amino acids 151-178 and a DP178-like hit at residues 426-512. ALLMOTI5 finds three areas including residues 117-182, 231-272, and 426-512. The hits from 426-512 include a region which is predicted by the Lupas method to have a high coiled-coil propensity (460-503). The PLZIP motifs identify only one region of interest at amino acids 273-289 (P1 and 12LZIPC).

15. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN HUMAN PARAINFLUENZA VIRUS

Both motifs 107x178x4 and ALLMOTI5 exhibit DP107-like hits in the same region, 115-182 and 117-182 respectively, of Human Parainfluenza Virus (strain NIH 47885; PC/Gene protein sequence name PVGLF\_p13H4;



(FIG. 25). In addition, the two motifs have a DP178-like hit just slightly C-terminal at amino acids 207-241. Both motifs also have DP178-like hits nearer the transmembrane region including amino acids 457-497 and 462-512 respectively. Several PLZIP motif hits are  
5 also observed including 283-303 (P5LZIPC), 283-310 (P12LZIPC), 453-474 (P6LZIPC), and 453-481 (P23LZIPC). The Lupas algorithm predicts that amino acids 122-176 may have a propensity to form a coiled-coil.

10 16. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP107-LIKE AND DP178-LIKE SEQUENCES OF  
INFLUENZA A VIRUS

FIG. 26 illustrates the Lupas prediction for a coiled coil in Influenza A Virus (strain A/Aichi/2/68)  
15 at residues 379-436, as well as the motif hits for 107x178x4 at amino acids 387-453, and for ALLMOTI5 at residues 380-456. Residues 383-471 (38-125 of HA2) were shown by Carr and Kim to be an extended coiled coil when under acidic pH (Carr and Kim, 1993, Cell  
20 73: 823-832). The Lupas algorithm predicts a coiled-coil at residues 379-436. All three methods successfully predicted the region shown to actually have coiled-coil structure; however, ALLMOTI5 predicted the greatest portion of the 88 residue  
25 stretch.

17. EXAMPLE: POTENTIAL RESPIRATORY SYNCYTIAL VIRUS  
DP178/DP107 ANALOGS: CD AND  
ANTIVIRAL CHARACTERIZATION

In the Example presented herein, respiratory  
30 syncytial virus (RSV) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 11, above, were tested for anti-RSV activity. Additionally, circular dichroism (CD) structural analyses were conducted on  
35 the peptides, as discussed below. It is demonstrated



that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of these peptides exhibit a substantial helical character.

5

#### 17.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a  
10 Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptides were synthesized according to the methods described, above, in Section 6.1. Peptide concentrations were determined from  $A_{280}$  using Edlehoch's method (1967, Biochemistry 6:1948).

15

Anti-RSV antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of HEP2 cells acutely infected with RSV (*i.e.*, cells which are infected with a multiplicity of infection of greater than 2) to fuse  
20 and cause syncytial formation on a monolayer of uninfected an uninfected line of Hep-2 cells. The lower the observed level of fusion, the greater the antiviral activity of the peptide was determined to be.

25

Uninfected confluent monolayers of Hep-2 cells were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes  
30 at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 3%, antibiotics (penicillin/streptomycin; Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

35

To prepare Hep2 cells for addition to uninfected cells, cultures of acutely infected Hep2 cells were



washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected Hep-2 cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Hep-2 cells, then adding peptides (at the dilutions described below) in 3% EMEM, and 100 acutely RSV-infected Hep2 cells per well. Wells were then incubated at 37°C for 48 hours.

After incubation, cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of either Crystal Violet stain or XTT. With respect to Crystal Violet, approximately 50µl 0.25% Crystal Violet stain in methanol were added to each well. The wells were rinsed immediately, to remove excess stain, and were allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

With respect to XTT (2,3-bis[2-Methoxy-4-nitro-5-sulfophenyl]-2H-tetrazolium-5-carboxyanilide inner salt), 50µl XTT (1mg/ml in RPMI buffered with 100mM HEPES, pH 7.2-7.4, plus 5% DMSO) were added to each well. The OD<sub>450/690</sub> was measured (after blanking against growth medium without cells or reagents, and against reagents) according to standard procedures.

**Peptides:** The peptides characterized in the study presented herein were:

1) peptides T-142 to T-155 and T-575, as shown in FIG. 27A, and peptides T-22 to T-27, T-68, T-334 and T-371 to T-375 and T-575, as shown in FIG. 27B;



- 2) peptides T-120 to T-141 and T-576, as shown in FIG. 27B, and peptides T-12, T-13, T-15, T-19, T-28 to T-30, T-66, T-69, T-70 and T-576, as shown in FIG. 27D; and
- 3) peptides T-67 and T-104 to T-119 and T-384, as shown in FIG. 28A, and peptides T-71, T-613 to T-617, T-662 to T-676 and T-730, as shown in FIG. 28B.

The peptides of group 1 represent portions of the RSV F2 protein DP178/107-like region. The peptides of group 2 represent portions of the RSV F1 protein DP107-like region. The peptides of groups 3 represent portions of the RSV F1 protein DP178-like region.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used. The IC<sub>50</sub> data for each peptide represents the average of several experiments conducted utilizing that peptide.

## 17.2 RESULTS

The data summarized in FIGS. 27A-B and 28A-B represent antiviral and structural information obtained from peptides derived from the RSV F2 DP178/DP107-like F2 region (FIG. 27A-B), the RSV F1 DP-107-like region (FIG. 27C-D) and the RSV DP178-like F2 region (FIG. 28A-B).

As shown in FIGS. 27A-D, a number of the RSV DP178/DP107-like peptides exhibited a detectable level of antiviral activity. Peptides from the RSV DP178/DP107-like F2 region (FIG. 27A-B), for example, T-142 to T-145 and T-334 purified peptides, exhibited detectable levels of antiviral activity, as evidenced by their IC<sub>50</sub> values. Further, a number of RSV F1 DP107-like peptides (FIG. 27C-D) exhibited a sizable level of antiviral activity as purified peptides, including, for example, peptides T-124 to T-127, T-



131, T-135 and T-137 to T-139, as demonstrated by their low  $IC_{50}$  values. In addition, CD analysis FIG. 27A, 27C) reveals that many of the peptides exhibit some detectable level of helical structure.

5 The results summarized in FIG. 28A-B demonstrate that a number of DP178-like purified peptides exhibit a range of potent anti-viral activity. These peptides include, for example, T-67, T-104, T-105 and T-107 to T-119, as listed in FIG. 28A, and T-665 to T-669 and T-671 to T-673, as listed in FIG. 28B. In addition,  
10 some of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, successfully identified viral peptide domains that represent highly promising anti-RSV  
15 antiviral compounds.

18. EXAMPLE: POTENTIAL HUMAN PARAINFLUENZA VIRUS  
TYPE 3 DP178/DP107 ANALOGS: CD AND  
ANTIVIRAL CHARACTERIZATION

20 In the Example presented herein, human parainfluenza virus type 3 (HPIV3) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 15, above, were tested for anti-HPIV3 activity.  
25 Additionally, circular dichroism (CD) structural analyses were conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of  
30 these peptides exhibit a substantial helical character.

18.1 MATERIALS AND METHODS

Structural analyses: Structural analyses  
35 consisted of circular dichroism (CD) studies. The CD



spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were  
5 determined from  $A_{220}$  using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-HPIV3 antiviral activity assays: The assay utilized herein tested the ability of the peptides to  
10 disrupt the ability of Hep2 cells chronically infected with HPIV3 to fuse and cause syncytial formation on a monolayer of an uninfected line of CV-1W cells. The more potent the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of CV-1W cells  
15 were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented  
20 at 3%, antibiotics/antimycotics (Gibco BRL Life Technologies Cat. No. 15040-017) added at 1%, and glutamine added at 1%.

To prepare Hep2 cells for addition to uninfected cells, cultures of chronically infected Hep2 cells  
25 were washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and  
30 resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected CV-1W cells.

The antiviral assay was conducted by, first,  
removing all media from the wells containing  
35 uninfected CV-1W cells, then adding peptides (at the



dilutions described below) in 3% EMEM, and 500 chronically HPIV3-infected Hep2 cells per well. Wells were then incubated at 37°C for 24 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Alternatively, instead of Crystal Violet analysis, cells were assayed with XTT, as described, above, in Section 17.1.

Peptides: The peptides characterized in the study presented herein were:

- 1) Peptides 157 to 188, as shown in FIG. 29A, and peptides T-38 to T-40, T-42 to T-46 and T-582, as shown in FIG. 29B. These peptides are derived from the DP107 region of the HPIV3 F1 fusion protein (represented by HPF3 107, as shown in FIG. 29A); and
- 2) Peptides 189 to 210, as shown in FIG. 30A, and T-269, T-626, T-383 and T-577 to T-579, as shown in FIG. 30B. These peptides are primarily derived from the DP178 region of the HPIV3 F1 fusion protein (represented by HPF3 178, as shown in FIG. 30A). Peptide T-626 contains two mutated amino acid residues (represented by a shaded background). Additionally, peptide T-577 represents F1 amino acids 65-100, T-578 represents F1 amino acids 207-242 and T-579 represents F1 amino acids 273-309.

Each peptide was tested at 2-fold serial dilutions ranging from 500µg/ml to approximately



500ng/ml. For each of the assays, a well containing no peptide was also used.

## 18.2 RESULTS

5 The data summarized in FIGS. 29A-B and 30A-B represent antiviral and structural information obtained from peptides derived from the HPIV3 fusion protein DP107-like region (FIG. 29A-B) and the HPIV3 fusion protein DP178-like region (FIG. 30A-B).

10 As shown in FIG. 29A-B, a number of the HPIV3 DP107-like peptides exhibited potent levels of antiviral activity. These peptides include, for example, peptides T-40, T-172 to T-175, T-178, T-184 and T-185.

15 The results summarized in FIG. 30A-B demonstrate that a number of the DP178-like peptides tested exhibit a range of anti-viral activity. These peptides include, for example, peptides 194 to 211, as evidenced by their low IC<sub>50</sub> values. In fact, peptides 201 to 205 exhibit IC<sub>50</sub> values in the nanogram/ml  
20 range. In addition, many of the DP178-like peptides exhibited some level of helicity.

25 Thus, the computer assisted searches described, hereinabove, have successfully identified viral peptide domains that represent highly promising anti-HPIV3 antiviral compounds.

### 19. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN IMMUNODEFICIENCY VIRUS

30 FIG. 31 represents search results for SIV isolate MM251 (PC/Gene® protein sequence PENV\_SIVM2). Both 107x178x4 and ALLMOTI5 search motifs identified two regions with similarities to DP107 and/or DP178.

35 The peptide regions found by 107x178x4 were located at amino acid residues 156-215 and 277-289. The peptide regions found by ALLMOTI5 were located at



amino acid residues 156-219 and 245-286. Both motifs, therefore, identify similar regions.

Interestingly, the first SIV peptide region (i.e., from amino acid residue 156 to approximately amino acid residue 219) correlates with a DP107 region, while the second region identified (i.e., from approximately amino acid residue 245 to approximately amino acid residue 289) correlates with the DP178 region of HIV. In fact, an alignment of SIV isolate MM251 and HIV isolate BRU, followed by a selection of the best peptide matches for HIV DP107 and DP178, reveals that the best matches are found within the peptide regions identified by the 107x178x4 and ALLMOTI5 search motifs.

It should be noted that a potential coiled-coil region at amino acid residues 242-282 is predicted by the Lupas program. This is similar to the observation in HIV in which the coiled-coil is predicted by the Lupas program to be in the DP178 rather than in the DP107 region. It is possible, therefore, that SIV may be similar to HIV in that it may contain a coiled-coil structure in the DP107 region, despite such a structure being missed by the Lupas algorithm. Likewise, it may be that the region corresponding to a DP178 analog in SIV may exhibit an undefined structure, despite the Lupas program's prediction of a coiled-coil structure.

30

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20. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN EPSTEIN-BARR  
VIRUS**

The results presented herein describe the identification of DP178/DP107 analogs within two different Epstein-Barr Virus proteins. Epstein-Barr is a human herpes virus which is the causative agent of, for example, infectious mononucleosis (IM), and is also associated with nasopharyngeal carcinomas (NPC), Burkitt's lymphoma and other diseases. The virus predominantly exists in the latent form and is activated by a variety of stimuli.

FIG. 32 depicts the search motif results for the Epstein-Barr Virus (Strain B95-8; PC/Gene® protein sequence PVGLB\_EBV) glycoprotein gp110 precursor (gp115). The 107x178x4 motif identified two regions of interest, namely the regions covered by amino acid residues 95-122 and 631-658. One PZIP region was identified at amino acid residue 732-752 which is most likely a cytoplasmic region of the protein. The Lupas algorithm predicts a coiled-coil structure for amino acids 657-684. No ALLMOTI5 regions were identified.

FIG. 33 depicts the search motif results for the Zebra (or EB1) trans-activator protein (BZLF1) of the above-identified Epstein-Barr virus. This protein is a transcription factor which represents the primary mediator of viral reactivation. It is a member of the b-ZIP family of transcription factors and shares significant homology with the basic DNA-binding and dimerization domains of the cellular oncogenes c-fos and C/EBP. The Zebra protein functions as a homodimer.

Search results demonstrate that the Zebra protein exhibits a single region which is predicted to be either of DP107 or DP178 similarity, and is found between the known DNA binding and dimerization regions of the protein. Specifically, this region is located



at amino acid residues 193-220, as shown in FIG. 33.  
The Lupas program predicted no coiled-coil regions.

21. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN MEASLES VIRUS

5 FIG. 34 illustrates the motif search results for  
the fusion protein F1 of measles virus, strain  
Edmonston (PC Gene® protein sequence PVGLF\_MEASE),  
successfully identifying DP178/DP107 analogs.

The 107x178x4 motif identifies a single region at  
10 amino acid residues 228-262. The ALLMOTI5 search  
motif identifies three regions, including amino acid  
residues 116-184, 228-269 and 452-500. Three regions  
containing proline residues followed by a leucine  
zipper-like sequence were found beginning at proline  
15 residues 214, 286 and 451.

The Lupas program identified two regions it  
predicted had potential for coiled-coil structure,  
which include amino acid residues 141-172 and 444-483.

20 22. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN HEPATITIS B  
VIRUS

FIG. 35 depicts the results of a PZIP motif  
search conducted on the Hepatitis B virus subtype AYW.  
Two regions of interest within the major surface  
25 antigen precursor S protein were identified. The  
first lies just C-terminal to the proposed fusion  
peptide of the major surface antigen (Hbs) which is  
found at amino acid residues 174-191. The second  
region is located at amino acid residues 233-267. The  
30 Lupas program predicts no coiled-coil repeat regions.

In order to test the potential anti-HBV antiviral  
activity of these D178/DP107 analog regions, peptides  
derived from area around the analog regions are  
synthesized, as shown in FIG. 52A-B. These peptides  
35 represent one amino acid peptide "walks" through the



putative DP178/DP107 analog regions. The peptides are synthesized according to standard Fmoc chemistry on Rinkamide MBHA resins to provide for carboxy terminal blockade (Chang, C.D. and Meinhofer, J., 1978, Int. J. Pept. Protein Res. 11:246-249; Fields, G.B. and Noble, R.L., 1990, Int. J. Pept. Protein Res. 35:161-214). Following complete synthesis, the peptide amino-terminus is blocked through automated acetylation and the peptide is cleaved with trifluoroacetic acid (TFA) and the appropriate scavengers (King, D.S. et al., 1990, Int. J. Pept. Res. 36:255-266). After cleavage, the peptide is precipitated with ether and dried under vacuum for 24 hours.

The anti-HBV activity of the peptides is tested by utilizing standard assays to determine the test peptide concentration required to cause an acceptable (e.g., 90%) decrease in the amount of viral progeny formed by cells exposed to an HBV viral inoculum. Candidate antiviral peptides are further characterized in model systems such as wood chuck tissue culture and animal systems, prior to testing on humans.

23. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN MASON-PFIZER MONKEY VIRUS

The results depicted herein illustrate the results of search motifs conducted on the Simian Mason-Pfizer monkey virus. The motifs reveal DP178/DP107 analogs within the enveloped (TM) protein GP20, as shown in FIG. 36.

The 107x178x4 motifs identifies a region at amino acid residues 422-470. The ALLMOTI5 finds a region at amino acid residues 408-474. The Lupas program predicted a coiled-coil structure a amino acids 424-459.



24. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS IN BACTERIAL  
PROTEINS**

5 The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to sequences present in proteins of a variety of bacterial species.

10 FIG. 37 depicts the search motif results for the *Pseudomonas aeruginosa* fimbrial protein (Pilin). Two regions were identified by motifs 107x178x4 and ALLMOTI5. The regions located at amino acid residues 30-67 and 80-144 were identified by the 107x178x4 motif. The regions at amino acid residues 30-68 and 80-125 were identified by the ALLMOTI5.

15 FIG. 38 depicts the search motif results for the *Pseudomonas gonorrhoeae* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 66-97 was identified by the 107x178x4 motif. The region located at amino acid residues 66-125 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

20 FIG. 39 depicts the search motif results for the *Hemophilus Influenza* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

25 FIG. 40 depicts the search motif results for the *Staphylococcus aureus* toxic shock syndrome *Hemophilus Influenza* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The



region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

5 FIG. 41 summarizes the motif search results conducted on the Staphylococcus aureus enterotoxin Type E protein. These results demonstrate the successful identification of DP178/DP107 analogs corresponding to peptide sequences within this protein, as described below.

10 The ALLMOTI5 motif identified a region at amino acid residues 22-27. The 107x178x4 motif identified two regions, with the first at amino acid residues 26-69 and the second at 88-115. A P12LZIPC motif search identified two regions, at amino acid residues 163-181 and 230-250.

15 The Lupas program predicted a region with a high propensity for coiling at amino acid residues 25-54. This sequence is completely contained within the first region identified by both ALLMOTI5 and 107x178x4 motifs.

20 FIG. 42 depicts the search motif results conducted on a second Staphylococcus aureus toxin, enterotoxin A. Two regions were identified by the ALLMOTI5 motif, at amino acid residues 22-70 and amino acid residues 164-205. The 107x178x4 motif found two  
25 regions, the first at amino acid residues 26-69 and the second at amino acid residues 165-192. A P23LZIPC motif search revealed a region at amino acid residues 216-250. No coiled-coil regions were predicted by the Lupas program.

30 FIG. 43 shows the motif search results conducted on the E. coli heat labile enterotoxin A protein, demonstrating that identification of DP178/DP107 analogs corresponding to peptides located within this protein. Two regions were identified by the ALLMOTI5  
35 motif, with the first residing at amino acid residues



55-115, and the second residing at amino acid residues 216-254. The 107x178x4 motif identified a single region at amino acid residues 78-105. No coiled-coil regions were predicted by the Lupas program.

5 25. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF  
DP178/DP107 ANALOGS WITHIN VARIOUS  
HUMAN PROTEINS**

The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to peptide sequences present within several different human proteins.

FIG. 44 illustrates the search motif results conducted on the human c-fos oncoprotein. The ALLMOTI5 motif identified a single region at amino acid residues 155-193. The 107x178x4 motif identified one region at amino acid residues 162-193. The Lupas program predicted a region at amino acid residues 148-201 to have coiled-coil structure.

FIG. 45 illustrates the search motif results conducted on the human lupus KU autoantigen protein P70. The ALLMOTI5 motif identified a single region at amino acid residues 229-280. The 107x178x4 motif identified one region at amino acid residues 235-292. The Lupas program predicted a region at amino acid residues 232-267 to have coiled-coil structure.

FIG. 46 illustrates the search motif results conducted on the human zinc finger protein 10. The ALLMOTI5 motif identified a single region at amino acid residues 29-81. The 107x178x4 motif identified one region at amino acid residues 29-56. A P23LZIPC motif search found a single region at amino acid residues 420-457. The Lupas program predicted no coiled-coil regions.



26. EXAMPLE: POTENTIAL MEASLES VIRUS DP178/DP107  
ANALOGS: CD AND ANTIVIRAL  
CHARACTERIZATION

In the Example presented herein, measles (MeV) virus DP178-like peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 21, above, are tested for anti-MeV activity. Additionally, circular dichroism (CD) structural analyses are conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that none of the these peptides exhibit a substantial helical character.

26.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from  $A_{280}$  using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-MeV antiviral activity syncytial reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of Vero cells acutely infected with MeV (*i.e.*, cells which are infected with a multiplicity of infection of 2-3) to fuse and cause syncytial formation on a monolayer of an uninfected line of Vero cells. The more potent the peptide, the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of Vero cells were grown in microtiter wells in 10% FBS EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum



[FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 10%, antibiotics/antimycotics (Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

To prepare acutely infected Vero cells for  
5 addition to the uninfected cells, cultures of acutely infected Vero cells were washed twice with HBSS (Bio Whittaker Cat. No. 10-543F) and cell monolayers were removed with trypsin (Bio Whittaker Cat. No. 17-161E).  
10 Once cells detached, media was added, any remaining clumps of cells were dispersed, and hemacytometer cell counts were performed.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the  
15 dilutions described below) in 10% FBS EMEM, and 50-100 acutely MeV-infected Vero cells per well. Wells were then incubated at 37°C for a maximum of 18 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the  
20 wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were  
25 then counted, using a dissecting microscope.

Anti-MeV antiviral activity plaque reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of MeV to infect permissive, uninfected Vero cells, leading to  
30 the infected cells' fusing with uninfected cells to produce syncytia. The lower the observed level of syncytial formation, the greater the antiviral activity of the peptide.

Monolayers of uninfected Vero cells are grown as  
35 described above.



The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and MeV stock virus at a final concentration of 30 plaque forming units (PFU) per well. Wells were then incubated at 37°C for a minimum of 36 hours and a maximum of 48 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Peptides: The peptides characterized in the study presented herein were peptides T-252A0 to T-256A0, T-257B1/C1, and T-258B1 to T-265B0, and T-266A0 to T-268A0, as shown in FIG. 47. These peptides represent a walk through the DP178-like region of the MeV fusion protein.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

## 26.2 RESULTS

The data summarized in FIG. 47 represents antiviral and structural information obtained via "peptide walks" through the DP178-like region of the MeV fusion protein.

As shown in FIG. 47, the MeV DP178-like peptides exhibited a range of antiviral activity as crude peptides. Several of these peptides were chosen for purification and further antiviral characterization.



The IC<sub>50</sub> values for such peptides were determined, as shown in FIG. 47, and ranged from 1.35µg/ml (T-257B1/C1) to 0.072µg/ml (T-265B1). None of the DP178-like peptides showed, by CD analysis, a detectable level of helicity.

5        Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-MeV antiviral compounds.

10

27. EXAMPLE:    POTENTIAL SIV DP178/DP107 ANALOGS:  
                 ANTIVIRAL CHARACTERIZATION

                 In the Example presented herein, simian immunodeficiency virus (SIV) DP178-like peptides  
15 identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9, 12 and 19, above, were tested for anti-SIV activity. It is demonstrated that several of the identified peptides exhibit potent antiviral  
20 capability.

27.1 MATERIALS AND METHODS

Anti-SIV antiviral assays: The assay utilized herein were as reported in Langolis et al. (Langolis,  
25 A.J. et al., 1991, AIDS Research and Human Retroviruses 7:713-720).

Peptides: The peptides characterized in the study presented herein were peptides T-391 to T-400, as shown in FIG. 48. These peptides represent a walk  
30 through the DP178-like region of the SIV TM protein.

                 Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

35



## 27.2 RESULTS

The data summarized in FIG. 48 represents antiviral information obtained via "peptide walks" through the DP178-like region of the SIV TM protein.

5 As shown in FIG. 48, peptides T-391 to T-400 were tested and exhibited a potent antiviral activity as crude peptides.

Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified  
10 viral peptide domains that represent highly promising anti-SIV antiviral compounds.

### 28. EXAMPLE: ANTI-VIRAL ACTIVITY OF DP107 AND DP- 178 PEPTIDE TRUNCATIONS AND MUTATIONS

15 The Example presented in this Section represents a study of the antiviral activity of DP107 and DP178 truncations and mutations. It is demonstrated that several of these DP107 and DP178 modified peptides exhibit substantial antiviral activity.

20

#### 28.1 MATERIALS AND METHODS

Anti-HIV assays: The antiviral assays performed were as those described, above, in Section 6.1. Assays utilized HIV-1/IIIB and/or HIV-2 NIH2 isolates.  
25 Purified peptides were used, unless otherwise noted in FIGS. 49A-C.

Peptides: The peptides characterized in the study presented herein were:

- 30 1) FIGS. 49A-C present peptides derived from the region around and containing the DP178 region of the HIV-1 BRU isolate. Specifically, this region spanned from gp41 amino acid residue 615 to amino acid residue 717. The peptides listed contain  
35 truncations of this region and/or mutations



which vary from the DP178 sequence amino acid sequence. Further, certain of the peptides have had amino- and/or carboxy-terminal groups either added or removed, as indicated in the figures; and

- 5           2) FIG. 50. presents peptides which represent truncations of DP107 and/or the gp41 region surrounding the DP107 amino acid sequence of HIV-1 BRU isolate. Certain of the peptides are unblocked or biotinylated, as indicated  
10           in the figure.

Blocked peptides contained an acyl N-terminus and an amido C-terminus.

## 28.2 RESULTS

15           Anti-HIV antiviral data was obtained with the group 1 DP178-derived peptides listed in FIG. 49A-C. The full-length, non-mutant DP178 peptide (referred to in FIG. 49A-C as T20) results shown are for 4ng/ml.

20           In FIG. 49A, a number of the DP178 truncations exhibited a high level of antiviral activity, as evidenced by their low  $IC_{50}$  values. These include, for example, test peptides T-50, T-624, T-636 to T-641, T-645 to T-650, T-652 to T-654 and T-656. T-50  
25           represents a test peptide which contains a point mutation, as indicated by the residue's shaded background. The HIV-1-derived test peptides exhibited a distinct strain-specific antiviral activity, in that none of the peptides tested on the HIV-2 NIHZ isolate demonstrated appreciable antti-HIV-2 antiviral  
30           activity.

35           Among the peptides listed in FIG. 49B, are test peptides representing the amino (T-4) and carboxy (T-3) terminal halves of DP178 were tested. The amino terminal peptide was not active ( $IC_{50} > 400 \mu g/ml$ ) whereas the carboxy terminal peptide showed potent antiviral



activity ( $IC_{50} = 3\mu g/ml$ ). A number of additional test peptides also exhibited a high level of antiviral activity. These included, for example, T-61/T-102, T-217 to T-221, T-235, T-381, T-677, T-377, T-590, T-378, T-591, T-271 to T-272, T-611, T-222 to T-223 and  
5 T-60/T-224. Certain of the antiviral peptides contain point mutations and/or amino acid residue additions which vary from the DP178 amino acid sequence.

In FIG. 49C, point mutations and/or amino and/or carboxy-terminal modifications are introduced into the  
10 DP178 amino acid sequence itself. As shown in the figure, the majority of the test peptides listed exhibit potent antiviral activity.

Truncations of the DP107 peptide (referred to in IG. 50 as T21) were also produced and tested, as shown  
15 in FIG. 50. FIG. 50 also presents data concerning blocked and unblocked peptides which contain additional amino acid residues from the gp41 region in which the DP107 sequence resides. Most of these peptides showed antiviral activity, as evidenced by  
20 their low  $IC_{50}$  values.

Thus, the results presented in this Section demonstrate that not only do the full length DP107 and DP178 peptides exhibit potent antiviral activity, but truncations and/or mutant versions of these peptides  
25 can also possess substantial antiviral character.

29: EXAMPLE: POTENTIAL EPSTEIN-BARR DP178/DP107  
ANALOGS: ANTIVIRAL CHARACTERIZATION

In the Example presented herein, peptides derived  
30 from the Epstein-Barr (EBV) DP-178/DP107 analog region of the Zebra protein identified, above, in the Example presented in Section 20 are described and tested for anti-EBV activity. It is demonstrated that among these peptides are ones which exhibit potential anti-  
35 viral activity.



## 29.1 MATERIALS AND METHODS

### Electrophoretic Mobility Shift Assays (EMSA):

Briefly, an EBV Zebra protein was synthesized utilizing SP6 RNA polymerase in vitro transcription and wheat germ in vitro translation systems (Promega Corporation recommendations; Butler, E.T. and Chamberlain, M.J., 1984, J. Biol. Chem. 257:5772; Pelham, H.R.B. and Jackson, R.J., 1976, Eur. J. Biochem. 67:247). The in vitro translated Zebra protein was then preincubated with increasing amounts of peptide up to 250 ng/ml prior to the addition of 10,000 to 20,000 c.p.m. of a <sup>32</sup>P-labeled Zebra response element DNA fragment. After a 20 minute incubation in the presence of the response element, the reaction was analyzed on a 4% non-denaturing polyacrylamide gel, followed by autoradiography, utilizing standard gel-shift procedures. The ability of a test peptide to prevent Zebra homodimer DNA binding was assayed by the peptide's ability to abolish the response element gel migration retardation characteristic of a protein-bound nucleic acid molecule.

Peptides: The peptides characterized in this study represent peptide walks through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. Specifically, the peptide walks covered the region from amino acid residue 173 to amino acid residue 246 of the EBV Zebra protein.

Each of the tested peptides were analyzed at a range of concentrations, with 150ng/ml being the lowest concentration at which any of the peptides exerted an inhibitory effect.

35



## 29.2 RESULTS

The EBV Zebra protein transcription factor contains a DP178/DP107 analog region, as demonstrated in the Example presented, above, in Section 20. This protein appears to be the primary factor responsible for the reactivation capability of the virus. A method by which the DNA-binding function of the Zebra virus may be abolished may, therefore, represent an effective antiviral technique. In order to identify potential anti-EBV DP178/DP107 peptides, therefore, peptides derived from the region identified in Section 20, above, were tested for their ability to inhibit Zebra protein DNA binding.

The test peptides' ability to inhibit Zebra protein DNA binding was assayed via the EMSA assays described, above, in Section 28.1. The data summarized in FIG. 51A-B presents the results of EMSA assays of the listed EBV test peptides. These peptides represent one amino acid "walks" through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. As shown in FIG. 51A-B, the region from which these peptides are derived lies from EBV Zebra protein amino acid residue 173 to 246. A number of the test peptides which were assayed exhibited an ability to inhibit Zebra protein homodimer DNA binding, including 439, 441, 444 and 445.

Those peptides which exhibit an ability to inhibit Zebra protein DNA binding represent potential anti-EBV antiviral compounds whose ability to inhibit EBV infection can be further characterized.

The present invention is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects



of the invention, and functionally equivalent methods  
and components are within the scope of the invention.  
Indeed, various modifications of the invention, in  
addition to those shown and described herein will  
become apparent to those skilled in the art from the  
5 foregoing description and accompanying drawings. Such  
modifications are intended to fall within the scope of  
the appended claims.

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WHAT IS CLAIMED IS:

1. An isolated peptide recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif.  
5
2. The peptide of Claim 1 wherein the peptide corresponds to a peptide present in a virus.
3. The peptide of Claim 2 in which the virus is  
10 HIV-1 or HIV-2.
4. The peptide of Claim 2 in which the virus is a respiratory syncytial virus.
- 15 5. The peptide of Claim 2 in which the virus is a human parainfluenza virus.
6. The peptide of Claim 2 in which the virus is an influenza virus.  
20
7. The peptide of Claim 2 in which the virus is a hepatitis B virus.
8. The peptide of Claim 2 wherein the virus is  
25 an Epstein-Barr virus.
9. A method for the inhibition of transmission of a virus to a cell, comprising contacting the cell with an effective concentration of a peptide  
30 recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif for an effective period of time so that no infection of the cell by the virus occurs.
10. The method of Claim 9 wherein the virus is  
35 HIV-1 or HIV-2.



11. The method of Claim 9 wherein the virus is a respiratory syncytial virus.

12. The method of Claim 9 wherein the virus is a human parainfluenza virus.

5

13. The method of Claim 9 wherein the virus is an influenza virus.

14. The method of Claim 9 in which the virus is a hepatitis B virus.

10

15. The method of Claim 9 wherein the virus is an Epstein-Barr virus.

15

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HIV1LAI (DP-178; SEQ ID:1)	YTSLIHSLIEESQNQOEKNEQELLELDKWASLWNWF
HIV1SF2 (DP-185; SEQ ID:3)	YTNTIYNLLEESQNQOEKNEQELLELDKWASLWNWF
HIV1RF (SEQ ID:4)	YTGIIYNLLEESQNQOEKNEQELLELDKWANLWNWF
HIV1MN (SEQ ID:5)	YTSIIYSLLEKSTQOEKNEQELLELDKWASLWNWF
HIV2ROD (SEQ ID:6)	LEANISKSLEQAQIQEKNMYELQKLNWDIFGNWF
HIV2NIHZ (SEQ ID:7)	LEANISQSLEQAQIQEKNMYELQKLNWDVFTNWL
DP180 (SEQ ID:2)	SSESFTLLEQWNNMKLQAEQHLEQINEKHYLEDIS
DP118 (SEQ ID:10)	QQLLDVVKRQOEMLRLTVWGTKNLQARVTAIEKYLKDQ
DP125 (SEQ ID:8)	CCGNNLLRAIEAQQHLLQLTVWG IKQLQARILAVERYLKDQ
DP116 (SEQ ID:9)	LQARILAVERYLKDQQQ

FIG.1



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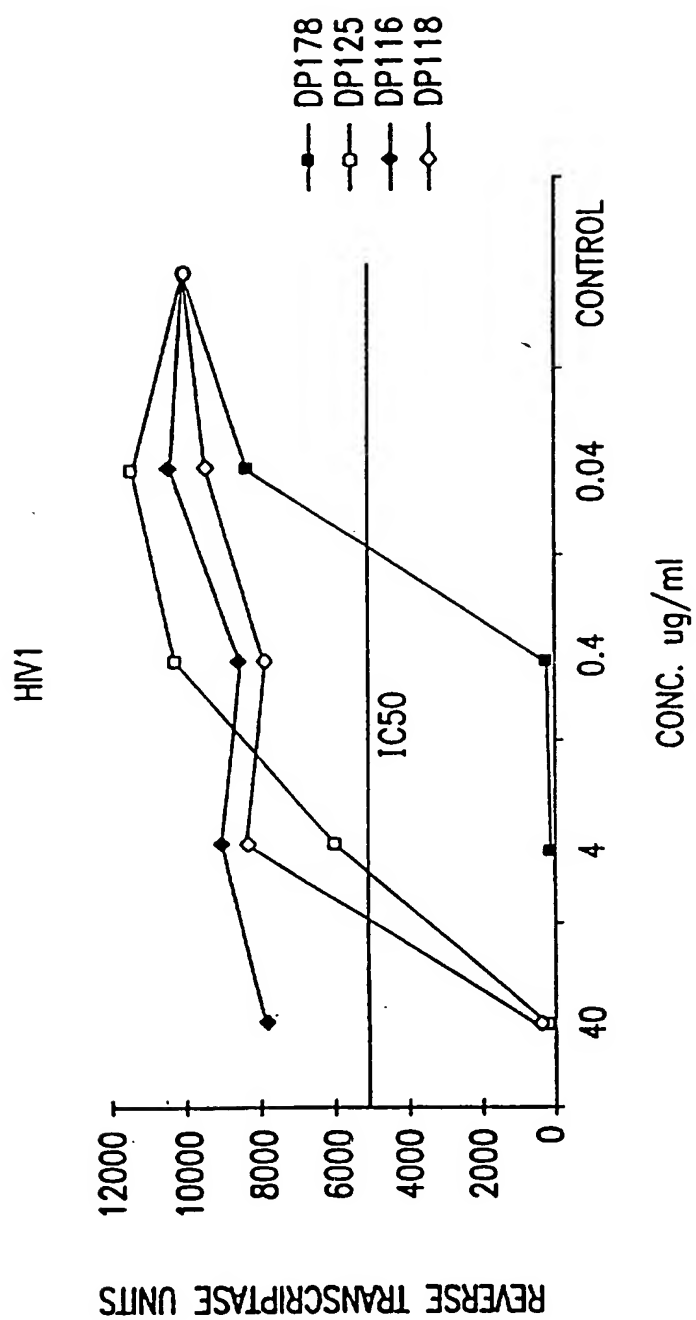


FIG.2



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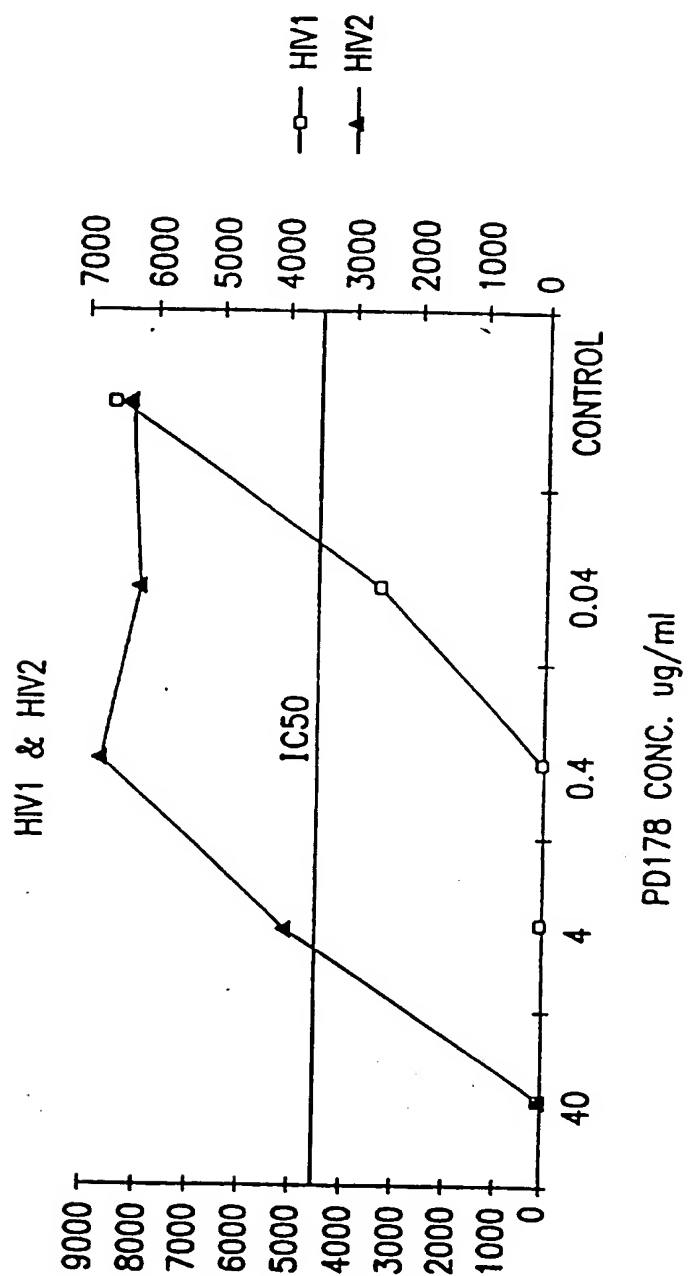


FIG.3



## 7872-020 (SHEET 4 OF 63)

Number of Syncytia/well: concentration in $\mu\text{g/ml}$ (micrograms/ml)									
DP178	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LAI	0	0	0	0	0	0	0	0	67
HIV1MN	0	0	0	0	0	ND	ND	ND	34
HIV1RF	0	0	0	0	0	ND	ND	ND	65
HIV1SF2	0	0	0	0	0	ND	ND	ND	58
DP125	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LAI	0	0	54	69	80	75	79	82	67
HIV1MN	0	0	30	36	ND	ND	ND	ND	34
HIV1RF	0	0	67	63	ND	ND	ND	ND	65
HIV1SF2	0	0	9	66	ND	ND	ND	ND	58
DP116	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LAI	75	ND	ND	ND	ND	ND	ND	ND	67
HIV1MN	35	ND	ND	ND	ND	ND	ND	ND	34
HIV1RF	81	ND	ND	ND	ND	ND	ND	ND	65
HIV1SF2	81	ND	ND	ND	ND	ND	ND	ND	58

FIG.4A

DP180	40	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncytia</i>									
HIV1LAI	50	>45	>45	>45	>45	>45	>45	>45	58
DP185	40	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncytia</i>									
HIV1LAI	0	0	0	0	0	0	0	ND	60

FIG.4B



## 7872-020 (SHEET 5 OF 63)

<u>HIV1</u>								
<u>Number of Syncytia/well: concentration in ng/ml (nanograms/ml)</u>								
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytia</u> <u>HIV1</u>	0	0	0	0	0	14	20	48
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytia</u> <u>HIV1</u>	ND	48	ND	ND	ND	ND	ND	ND
<u>HIV2</u>								
<u>Number of Syncytia/well: concentration in <math>\mu</math>g/ml (micrograms/ml)</u>								
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytia</u> <u>HIV2</u>	50	54	55	57	63	77	78	76
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytia</u> <u>HIV2</u>	ND	58	ND	ND	ND	ND	ND	ND

FIG.5



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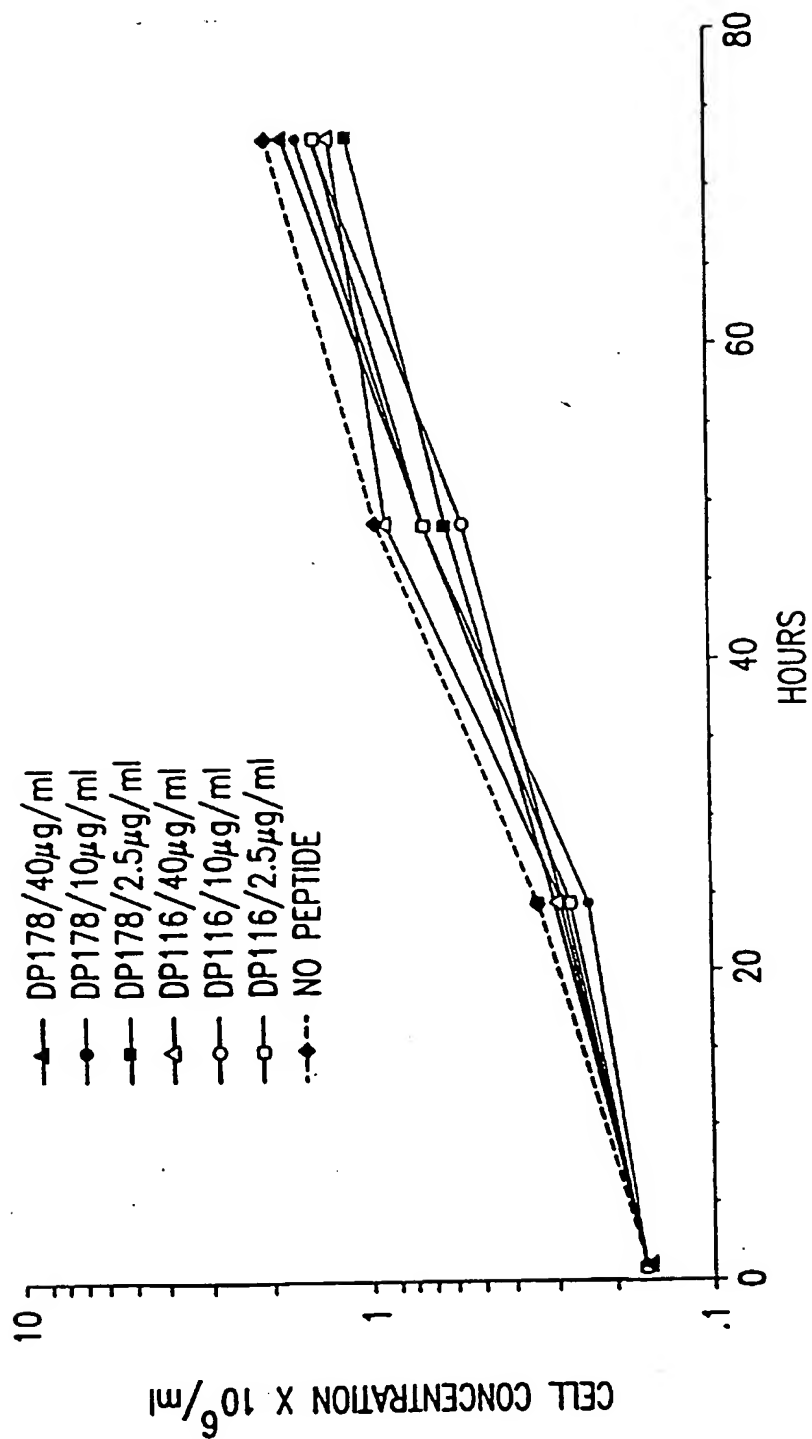


FIG. 6



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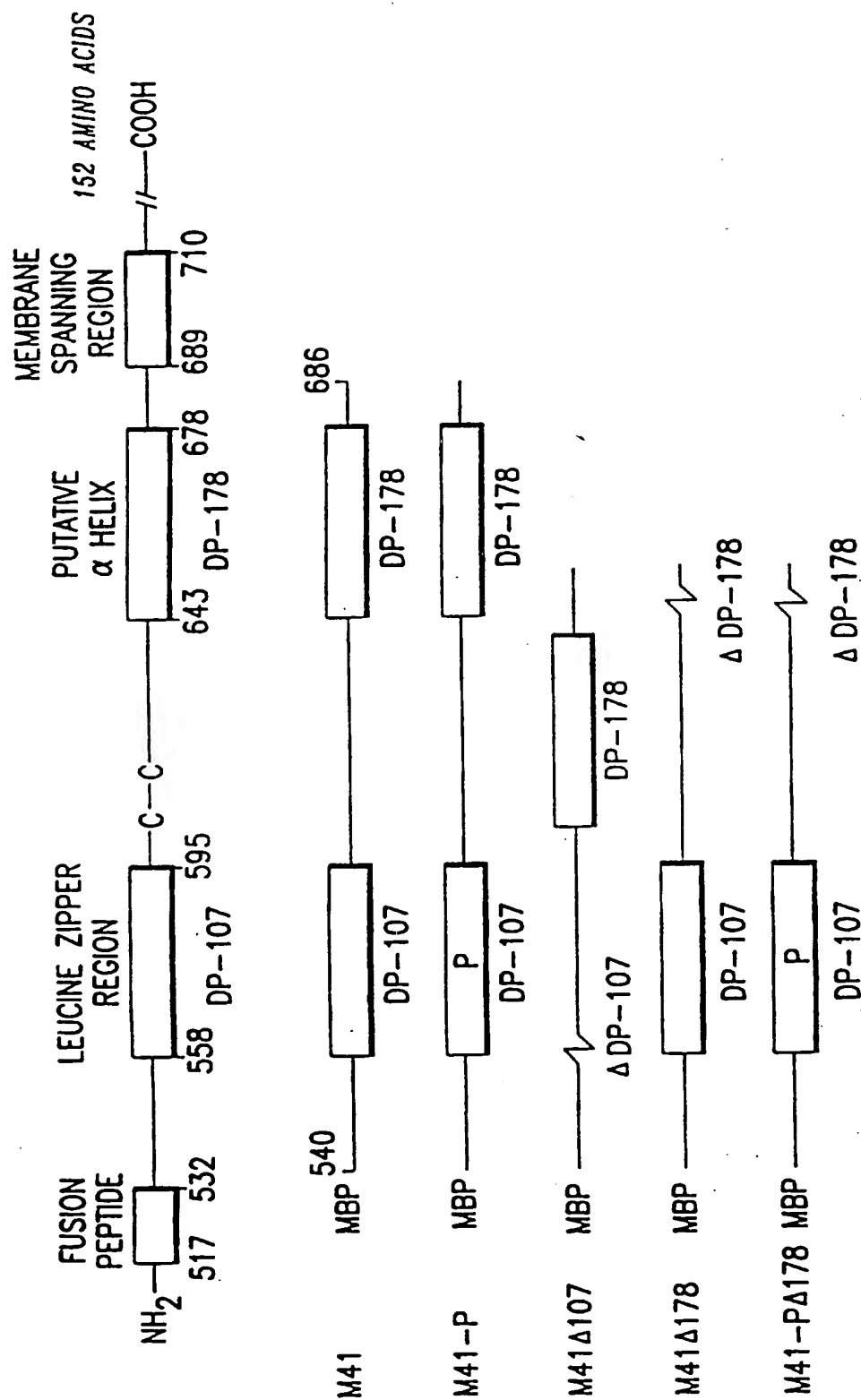


FIG. 7



7872-020 (SHEET B OF 63)

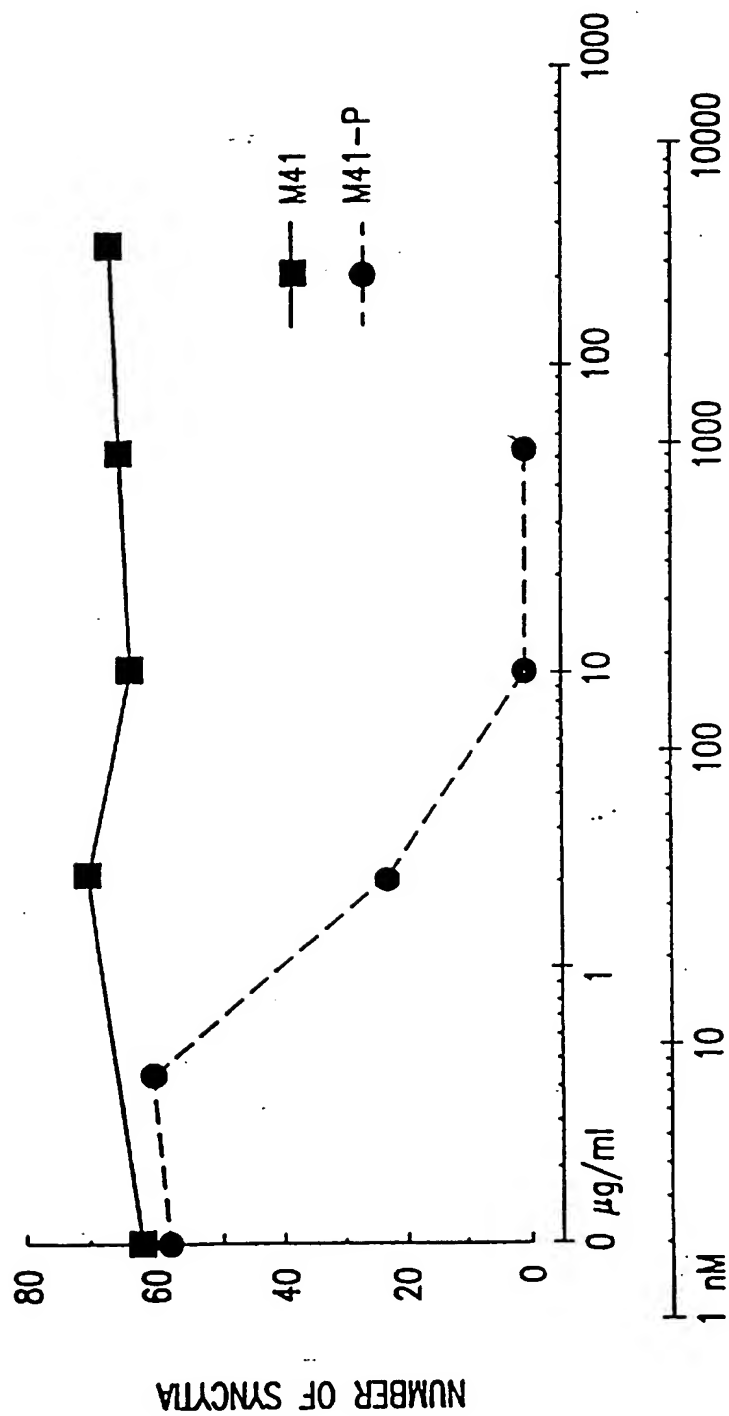


FIG.8



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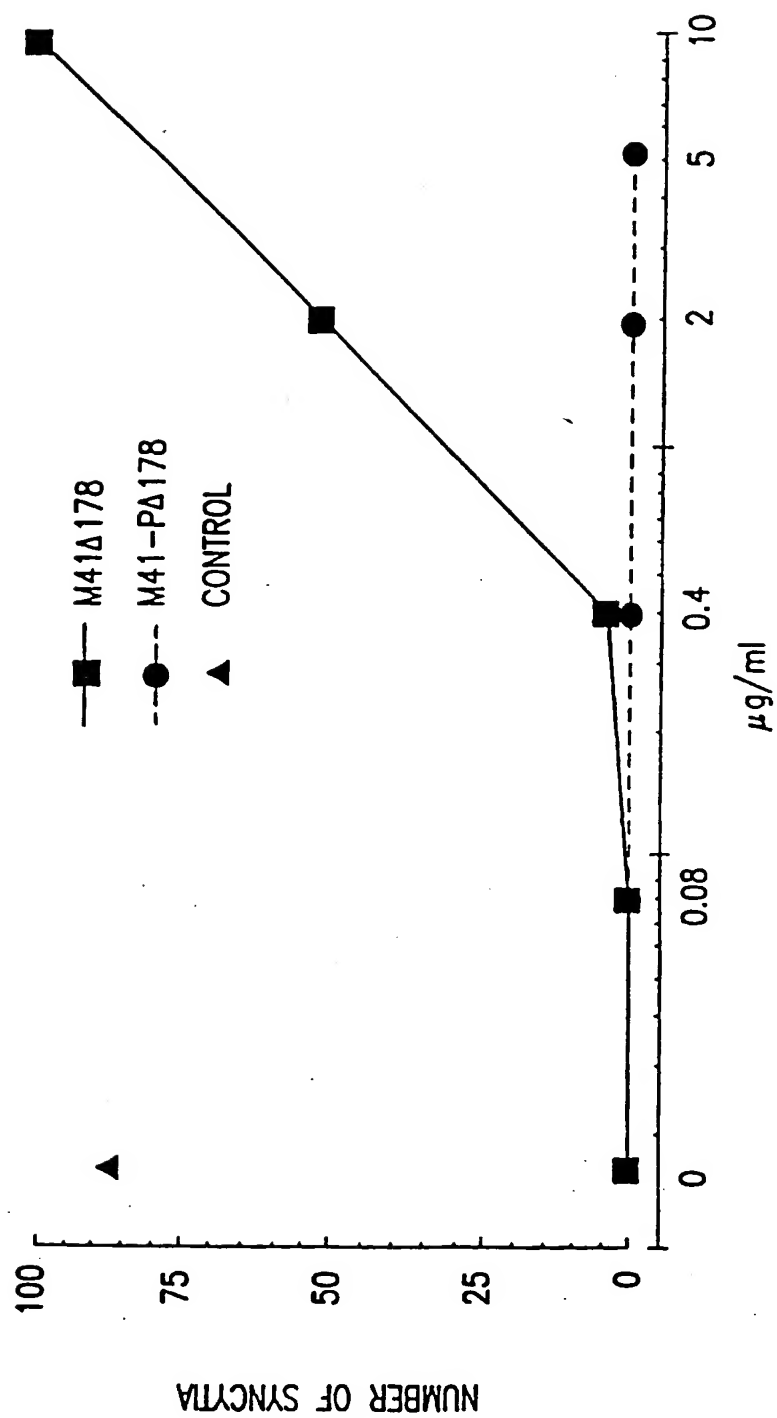


FIG.9



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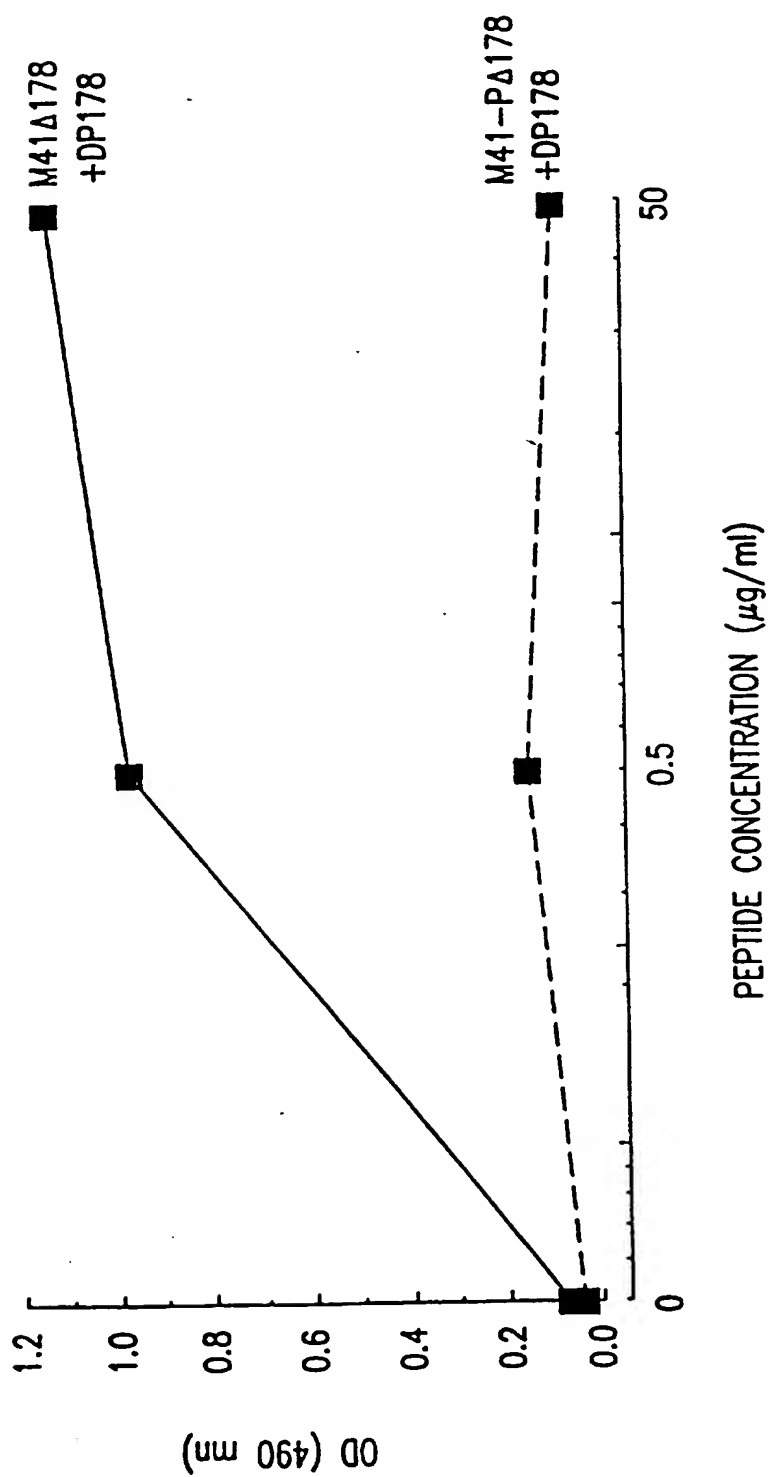


FIG.10



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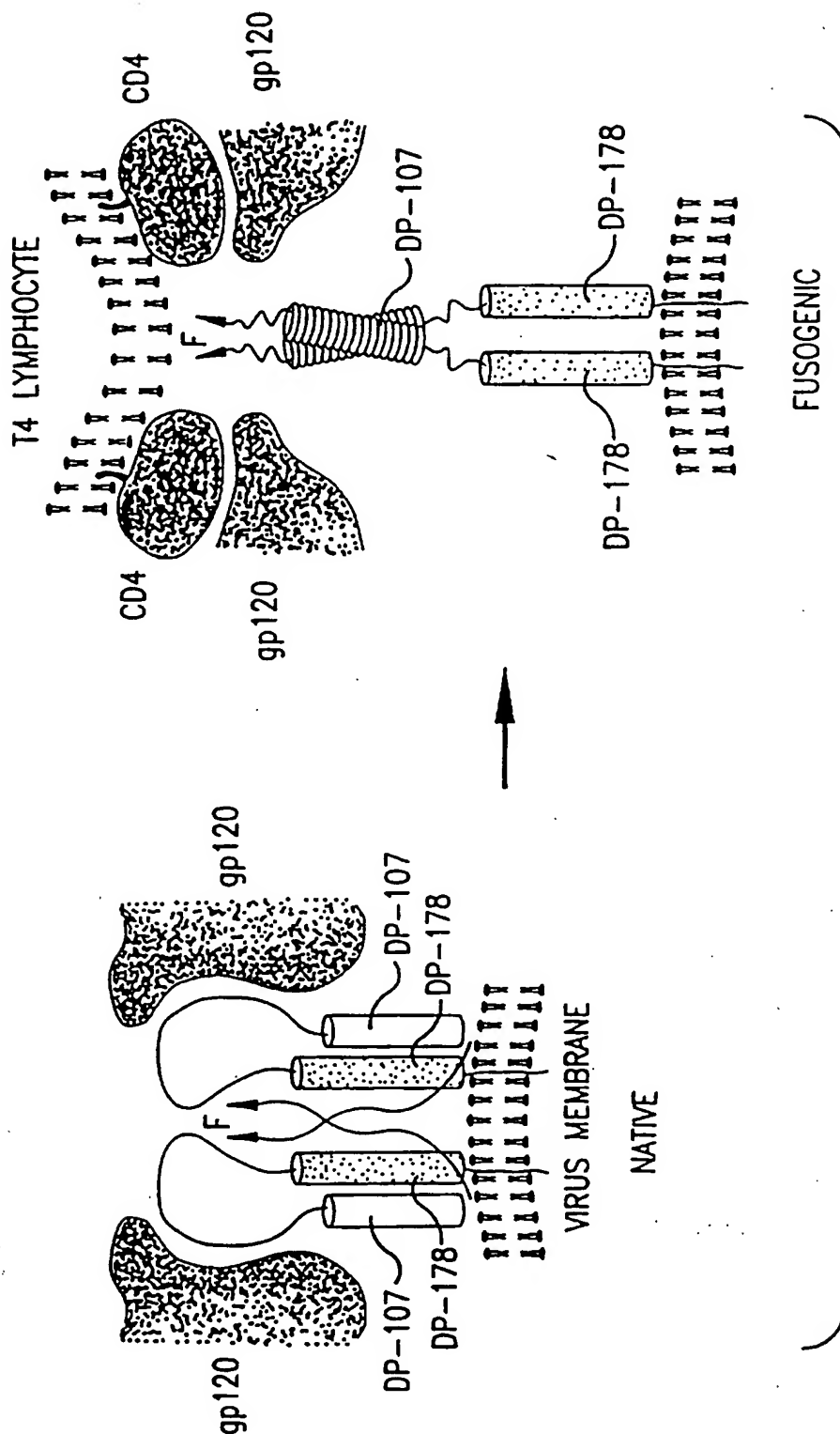
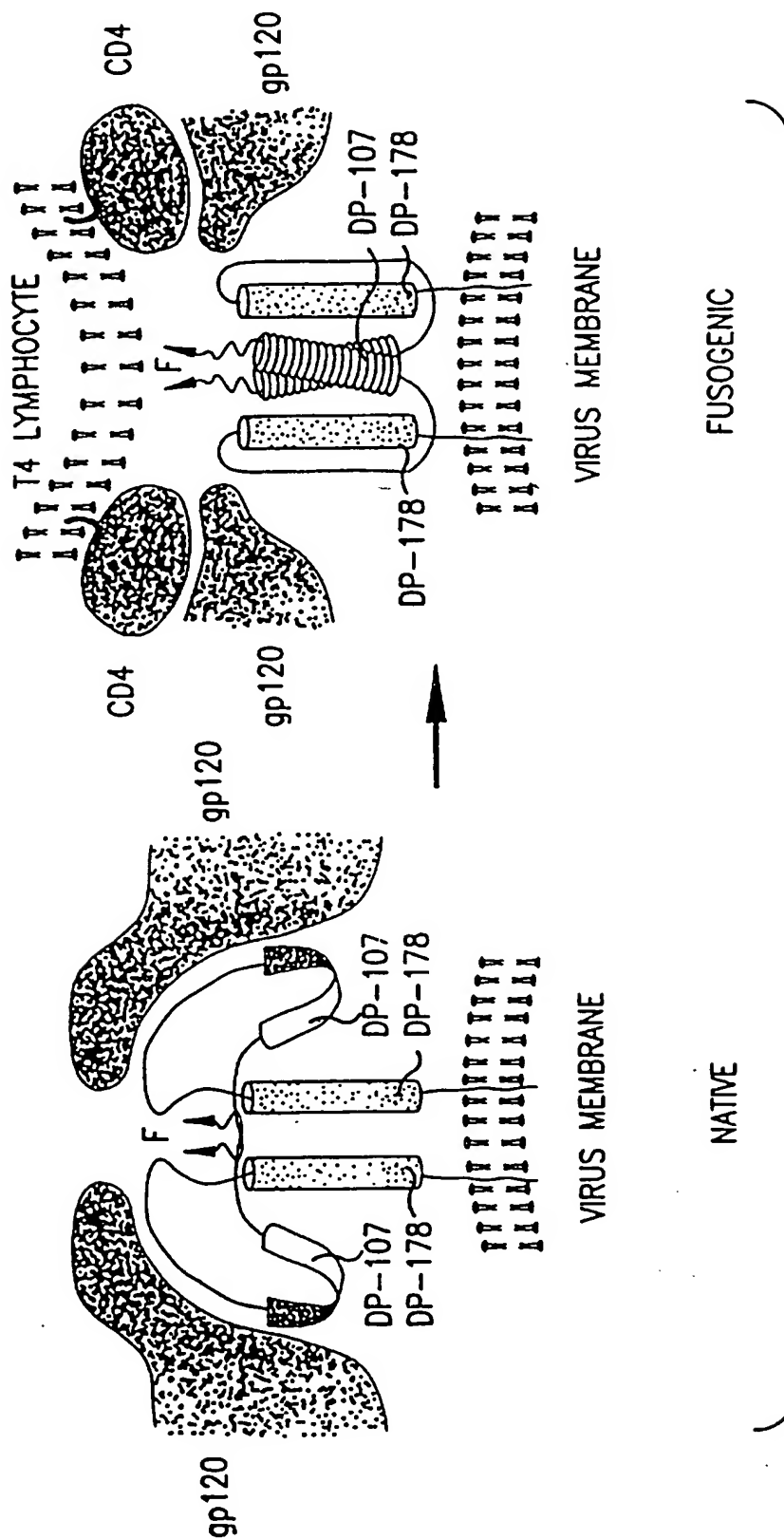


FIG.11A



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Sequence	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	Motifs
GCN4 (gcn4 yeast)	M	K	Q	L	E	D	K	V	E	E	L	L	S	K	N	Y	H	L	{LMNV} {CFGIMPVH}
C-FOS (fos_human)	T	D	T	L	Q	A	E	T	D	Q	L	E	D	E	K	S	A	L	{IKLT} {CFGIMPVH}
C-JUN (lap1_human)	I	A	R	L	E	E	K	V	K	T	L	K	A	Q	N	S	E	L	{AILNV} {CDFGHILPVH}
C-MYC (myo_human)	E	Q	K	L	I	S	E	E	D	L	L	E	K	R	E	Q	L	E	{ELR} {ACFGMPVH}
FLU LOOP 36	I	E	K	T	N	E	K	F	H	Q	I	E	K	E	F	S	E	V	{FILTV} {ACFLMPTVH}

FIG.12



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Sequence	Positions												Motifs
	A	D	A	D	A	D	A	D	A	D	A	D	
DP-107 (env_hv1bru) L1=D	N	L	L	R	A	I	E	A	Q	H	L	L	{ILQT} {CFIMPSTY}
DP-107 (env_hv1bru) L1=D	N	L	L	R	A	I	E	A	Q	H	L	L	{ILQTV} {CDFIMPST}
DP-107 (env_hv1bru) L1=D	N	L	L	R	A	I	E	A	Q	H	L	L	{ILQTV} {CDFIMPST}
DP-107 (env_hv1bru) L2=D	N	L	L	R	A	I	E	A	Q	H	L	L	{EKLNOV} {COFKMPSTY}
DP-107 (env_hv1bru) L2=D	N	L	L	R	A	I	E	A	Q	H	L	L	{EKLNOV} {CFKMPST}
DP-107 (env_hv1bru) L2=D	N	L	L	R	A	I	E	A	Q	H	L	L	{EKLNOV} {CFKMPST}
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	E	S	{EKLQY} {ACFGMPRWY}
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	E	S	{EKLQY} {CFGMPRVY}
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	E	S	{EFKLQY} {CFGMPRVY}
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	{EILNOSY} {ACFGMPRWY}
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	{EILNOSY} {CFGMPRVY}
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	{EFILNOSY} {CFGMPRVY}

FIG.13











7872-020 (SHEET 17 OF 63)

Sequence	Positions																								Parent Motif	Hybrid Motif									
	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D					
DP-107 (env_hv1bru) L1=D	N	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	W	G	I	K	Q	L	A	V	E	R	Y	L	K	D	D	[ILQIV] {CDFIMPST}		
DP-107 (env_hv1bru) L2=D	N	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	W	G	I	K	Q	L	A	V	E	R	Y	L	K	D	D	[EKLNV] {CFKAPS}		
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	E	K	N	E	Q	E	L	L	E	L	D	K	W	A	S	L	W	N	W	F	[EFKLOHY] {CFGLPRVY}
DP-178 (env_hv1bru) Y1=D			Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	E	K	N	E	Q	E	L	L	D	K	W	A	S	L	W	N	W	F	[EFILNDSHY] {CFGLPRVY}
FLU LOOP 36	I	E	K	T	N	E	K	F	H	O	I	E	K	E	F	S	E	V	E	G	R	I	Q	D	L	E	K	Y						[FILTV] {ACFLMPTWY}	

FIG.16



## 7872-020 (SHEET 18 OF 63)

Sequence	Positions																Parent Motif	Hybrid Motif	
	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D			
GCN4 (gcn4 yeast)	M	K	Q	L	E	D	K	V	E	E	L	S	K	N	Y	H	L	[LNAV] {CFGIMPW}	
DP-107 (env_hv1bru)L1=D	N	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	[ILOTV] {CDFIMPST}	
DP-178 (env_hv1bru)Y1=A	Y	T	S	L	I	M	S	L	I	E	E	S	N	Q	Q	E	K	[EFKLOWY] {CFGPRVY}	[EFIKLANDVWY] {CFMP}
GCN4 (gcn4 yeast)	M	K	Q	L	E	D	K	V	E	E	L	S	K	N	Y	H	L	[LNAV] {CFGIMPW}	
DP-107 (env_hv1bru)L1=D	N	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	[ILOTV] {CDFIMPST}	
DP-178 (env_hv1bru)Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	N	Q	Q	E	K	[EFILNDSWY] {CFGPRVY}	[EFILANDRSTWY] {CFMP}
GCN4 (gcn4 yeast)	M	K	Q	L	E	D	K	V	E	E	L	S	K	N	Y	H	L	[LNAV] {CFGIMPW}	
DP-107 (env_hv1bru)L2=D	N	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	[EKLNV] {CFKAPS}	
DP-178 (env_hv1bru)Y1=A	Y	T	S	L	I	H	S	L	I	E	E	S	N	Q	Q	E	K	[EFKLOWY] {CFGPRVY}	[EFKLANDVWY] {CFMP}
GCN4 (gcn4 yeast)	M	K	Q	L	E	D	K	V	E	E	L	S	K	N	Y	H	L	[LNAV] {CFGIMPW}	
DP-107 (env_hv1bru)L2=D	N	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	[EKLNV] {CFKAPS}	
DP-178 (env_hv1bru)Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	N	Q	Q	E	K	[EFILNDSWY] {CFGPRVY}	[EFIKLANDSWY] {CFMP}

FIG.17



7872-020 (SHEET 19 OF 63)

Sequence	Positions																Parent Motif	Hybrid Motif
	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D		
GCN4 (gcN4 yeast)	M	K	Q	L	E	D	K	V	E	E	L	L	S	K	N	I	{LIMV} {CFGIMPVW}	
DP-107 (env_hv1bru) L1=D	N	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	L	{ILOTV} {CDFIMPST}	
DP-107 (env_hv1bru) L2=D	N	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	L	{EKLNV} {CFGKPS}	
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	E	E	{EFKLVY} {CFGPRVY}	
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	E	E	{EFILNDSWY} {CFGPRVY}	
C-FOS (fos_human)	T	D	T	L	Q	A	E	T	D	Q	L	E	D	E	K	S	{IKLT} {CFGIMPVW}	
C-JUN (lop1_human)	I	A	R	L	E	E	K	V	K	T	L	K	A	Q	N	S	{AILNV} {CDFCHILPVW}	
C-MYC (myo_human)	E	Q	K	L	I	S	E	E	D	L	L	E	K	R	R	E	{ELR} {ACFGPVW}	
FLU LOOP 36	I	E	K	T	N	E	K	F	H	Q	I	E	K	F	S	E	{FILTV} {ACFLIPTW}	
																	{AEFIKLNQSTVWY} {CFPI}	
																	= {CCGIP} {CFPI}	

FIG.18



7872-020 (SHEET 20 OF 63)

P-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(1)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(2)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(3)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(4)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(5)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(6)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(7)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(8)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(9)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-{P}(10)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-X(1,12)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]  
 P-X(13,23)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]

FIG.19







## 7872-020 (SHEET 22 OF 63)

Fusion                    ♡ALLMOTIS♡  
 Peptide                   ♡107x178x4♡  
 ♡.....FLGFL      LGVGSALAS GVA   ♡VSKVLHLEGEVNIQKSA

                                 ♡P1&12LZIPC♡  
LLSTNKAVVLSNGVSVLTSKYLDLKNYIDKQ ♡ ♡ LL ♡PIVNKQ

                 ♡107x178x4♡  
 SC ♡SISNIETV ♡ EFOQKNRLLRETSYNAG ♡ VTPVSTMLTNSELLSL

                 ♡P1&12LZIPC♡  
                  ♡ALLMOTIS♡  
 INDM ♡PI ♡TNDQKKLMSNNVQI ♡V ♡ RQSYSI ♡ MSIIKEEVLAYV

VQ ♡ LPLYGVIDTPCWKLHTSP LCTTNTKEGS NICLTRTDRG WYCDNAGSVS

FFPQAETCKV QSNRVFCDTM NSLTLPSEIN LCNVDIFNPK

YDCKIMTSKT DVSSSVITSL GAIVSCYGKT KCTASNKNRG

IIKTFSNGCDYVSNKGMDTV SVGNTLYYVN KQEGKSLYVK G

                 ♡P7, 12, & 23LZIPC♡  
                  ♡107x178x4♡                   ♡ALLMOTIS♡  
 EPIINFYDPLVF ♡PSDE ♡EDASISQVNEKINOSLAF ♡I ♡ RKSDELL ♡

                 ♡Transmembrane Region♡  
HNVNA ♡ GKSTTN ♡IMTTTITVIVILLSLIAVGLLLY ♡ C ♡

KARSTPVTLS KDQLSGINNI AFSN

FIG. 21



## 7872-020 (SHEET 23 OF 63)

Fusion  
 Peptide      ♡ALLMOTIS♡      ♡107x178x4♡  
 .....FLGFLG      ♡AAGTAMGAAA      ♡TALTYQSOHLLAGILOQQKNLLAAV

♡107x178x4♡  
EAQ ♡ QQM ♡ LKLTIWGVKNLNARVTALEKYLEDOARLN ♡ AWG ♡ CA

♡LVS Coiled-Coil♡  
 ♡ALLMOTIS♡      ♡107x178x4♡  
 WKQVCHTTVP WQWNNRTPDW ♡NNMT ♡WLE ♡WEROISYLEGNIT

♡107x178x4♡  
TOLEEARAQEEKNLD ♡ AYOKLSS ♡ WSDFWSW ♡ FDF ♡SKWLN ♡ILK

♡Transmembrane Region♡  
IGELDYLGIGLRLLYTV ♡ YS ♡ CIARVRQGYS PLSPQIHHP WKGQPDNAEG

PGEKGDKRKN SSEPWQKESG TAEWKSNNWCK RLTNWCSISS IWLKNS

♡ALLMOTIS♡  
 ♡CLTL LVHLRSAFQY IQYGLGELKA AAQEAVVALA RLAQNAGYQIWL♡

ACRSAYRA IINSPRRVRQ GLEGILN

FIG. 22



## 7872-020 (SHEET 24 OF 63)

Fusion +107x178x4+  
 Peptide \*LVS Coiled-Coil\*  
 .....EAG +\*SNLNAQAIQ  
▼ALLMOTIS▼  
▼VYL AGVALGVATA AQITAGIALHQ

SLRTSLEQSNKAIEEIREATOETVIA\* VOGVODY+ VNNEL▼ VP

▼ALLMOTIS▼  
 +107x178x4+

AMQHMSCELVGQRLGLRLLRYYTELLSIFGPSLRD +P6 & 12LZIPC+  
 +PISA +▼EISIQALIVAL

GGEIHKLEKLGXSGSD+ MIALESRGIKTKI▼ THVDLPGKF ILSISY

+P1 & 12LZIPC+  
 +PTLSEVKGVIVHRLEAV+ SYNIGSQEWYTTVPRIATNGYLISNFDDESSCVFVS

ESAICSQNSL YPMSPLLQQC IRGDTSSCAR TLVSGTMGNK FILSKGNIVA

NCASILCKCY STSTINQSP DKLLTFIASD TCPLVEIDGA TIQVGGRQYP

\*LVS Coiled-Coil\*  
 ▼ALLMOTIS▼

+P12 & 23LZIPC+  
 DMVYEGKVAL G +PAISLD ▼RL\*DVGTNLGNALKIKLDDAKVLI+

♦Transmembrane Region♦

DSS+ NOILETVR RS▼\* SFN ♦EGSLLSVPILSCTALALLLLYCC♦

K RRYQQTLKQH TKVDPAFKPD LTGTSKSYVR SL

FIG. 23



## 7872-020 (SHEET 25 OF 63)

Fusion ♡ALLMOTI5♡  
 Peptide ♡107x178x4♡  
 ♡.....EIGAI IGSVALGVA TAAQITAASA LIQANQNAAN ♡ILRLKESITA

TIEAVHIEYTDGLSOLAVA ♡ VG KM ♡ QQFVNDQFNNTAQELDCIKITQQV

♡ALLMOTI5♡  
 GVELNLYLTELTIV FGPQITSPAL ♡TQLTIQALYNAGGNMDYLLTKLGVG

♡P1 & 12LZIPC♡  
 NNQLSSLIGSGLIT GN ♡ ♡PILYDSQT QLLGIQVTLP SVGNLNNMRATYLET

LSVST TKGFASALVP KVVVTQVGSVI EELDTSYCIE TDLDLYCTRI VTFPMSPGIY

SCLNGNTSAC MYSKTEGALT TPYMTLKGSV IANCKMTTCR CADPPGIISQ

♡ALLMOTI5♡  
 ♡107x178x4♡  
 NYGEAVSLID RHSCN ♡ ♡VLSLD GITRLSGEF DATYQKNISI LDSQVIVTG

♡LVS Coiled-Coil♡ ♡Trans-  
 ♡NLDISTELGNY NNSISNALDK LEESNSKLDK VNVKLTSTSA ♡LIT ♡VIA

membrane Region ♡  
LTALSLVCGITSLV ♡ ♡LACYLMY ♡ KQKAQQKTLLWLGNNTLGQMRATTKM

FIG. 24



## 7872-020 (SHEET 26 OF 63)

Fusion                    ♡ALLMOTIS♡  
 Peptide           ♡107x178x4♡    \*LVS Coiled-Coil\*  
 .....EEGGV    ♡IG ♡TIALG ♡VATSAQITA AVALVEAKOARSDIEKLKE

AIRDTNKA VOSV OSSIGNLIVA IKS VQ\* DYVNKE♡ ♡ IVPSIARLGCEAAG

                 ♡ALLMOTIS♡  
                  ♡107x178x4♡  
 LQLGIALTQH ♡♡YSELTNIEGDNIGSLOEKG I KLOGIASLYRTNITE♡ ♡

                                 ♡P5 & 12LZIPC♡  
 IFTTSTVDKYDIYDLLFTESIKVRVIDVDLNDYSITLQVRL ♡PLLTRLNLTQIYR

VDSISYNI♡ QNREWI♡ PLPSHIMTKGAFLGGADVKECIEAFSSYIC

PSDPGFVLNHEMESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITT

TCTCNGIGNRINQPPDQGVKIITHKECNTIGINGMLFNTNKEGTLAFYTP

                 ♡ALLMOTIS♡  
                  ♡107x178x4♡  
                  ♡P6 & 23LZIPC♡  
 NDITLNNVALD ♡PIDI ♡SIELN ♡KAKSDLEESKEWI♡ RRSNOKL÷

                 ♡Transmembrane Region♡  
DSIGNWHO SSTT ♡IIIV♡ LIM I I L F I I N V T I I♡ IIAVKYY♡ R

IQKRNRVDQN DKPYVLTK



7872-020 (SHEET 27 OF 63)

Fusion  
Peptide  
.....GLFGAI AGFIENGWEGMIDGWYGRHQNSEGTG

♣107x178x4♣

♥ALLMOTIS♥

\*LVS Coiled-Coil\*\*Q ♥AADLKST ♣QAAIDQINGKLNRYIEKTNEKTHQIEKEESEVEGRIODLEKYVEDTKIDL\* WSYNAELLYALENQHTI♣ DLT♥ DSEMKNLFETR

RQLRENAEEMGNGCFKIYHKCDNACIESIRNGTYDHDVYRDEALNNRFQIKG

VELKSGYKDWILWISFAISCFLLCVVLLGFIMWACQRGNIRCNICI

FIG. 26



7872-020 (SHEET 28 OF 63)



7872-020 (SHEET 29 OF 63)

RSV	Peptide #	AVG. IC50 (XTT) ug/ml
T-22	IELSNIKEHNKCNQTDAKVVKLLIKQELDKYKNAVT	>500
T-23	IELSNIKEHNKCNQTDAKVVKLLIKQELDKYKNAVT	>500
T-24	IELSNIKEHNKCNQTDAKVVKLLIKQELDKYKNAVT	>500
T-25	IELSNIKEHNKCNQTDAKVVKLLIKQELDKYKNAVT	>500
T-26	IELSNIKEHNKCNQTDAKVVKLLIKQELDKYKNAVT	>500
T-27	IELSNIKEHNKCNQTDAKVVKLLIKQELDKYKNAVT	>500
T-68	VSKGYBALRTQWYTBVITIELSNIKEN	165
T-334	AFIRKSDLELLHNV	26
T-371	YTBVITIELSNIKENKUNQTDAKVVKLLIKQELDKYKNAVT	>500
T-372	YTBVITIELSNIKENKUNQTDAKVVKLLIKQELDKYKNAVT	NOT TESTED
T-373	YTBVITIELSNIKENKUNQTDAKVVKLLIKQELDKYKNAVT	>500
T-374	YTBVITIELSNIKENKUNQTDAKVVKLLIKQELDKYKNAVT	>500
T-375	YTBVITIELSNIKENKUNQTDAKVVKLLIKQELDKYKNAVT	>500
T-575	AVSKGYBALRTQWYTBVITIELSNIKENKUNQTD	>100

FIG. 27B



7872-020 (SHEET 30 OF 63)

RSV DP-107-LIKE REGION (F1)																										Period										Periodicity																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
RSV	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000	1001	1002	1003	1004	1005	1006	1007	1008	1009	1010	1011	1012	1013	1014	1015	1016	1017	1018	1019	1020	1021	1022	1023	1024	1025	1026	1027	1028	1029	1030	1031	1032	1033	1034	1035	1036	1037	1038	1039	1040	1041	1042	1043	1044	1045	1046	1047	1048	1049	1050	1051	1052	1053	1054	1055	1056	1057	1058	1059	1060	1061	1062	1063	1064	1065	1066	1067	1068	1069	1070	1071	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090	1091	1092	1093	1094	1095	1096	1097	1098	1099	1100	1101	1102	1103	1104	1105	1106	1107	1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	1119	1120	1121	1122	1123	1124	1125	1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148	1149	1150	1151	1152	1153	1154	1155	1156	1157	1158	1159	1160	1161	1162	1163	1164	1165	1166	1167	1168	1169	1170	1171	1172	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1185	1186	1187	1188	1189	1190	1191	1192	1193	1194	1195	1196	1197	1198	1199	1200	1201	1202	1203	1204	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227	1228	1229	1230	1231	1232	1233	1234	1235	1236	1237	1238	1239	1240	1241	1242	1243	1244	1245	1246	1247	1248	1249	1250	1251	1252	1253	1254	1255	1256	1257	1258	1259	1260	1261	1262	1263	1264	1265	1266	1267	1268	1269	1270	1271	1272	1273	1274	1275	1276	1277	1278	1279	1280	1281	1282	1283	1284	1285	1286	1287	1288	1289	1290	1291	1292	1293	1294	1295	1296	1297	1298	1299	1300	1301	1302	1303	1304	1305	1306	1307	1308	1309	1310	1311	1312	1313	1314	1315	1316	1317	1318	1319	1320	1321	1322	1323	1324	1325	1326	1327	1328	1329	1330	1331	1332	1333	1334	1335	1336	1337	1338	1339	1340	1341	1342	1343	1344	1345	1346	1347	1348	1349	1350	1351	1352	1353	1354	1355	1356	1357	1358	1359	1360	1361	1362	1363	1364	1365	1366	1367	1368	1369	1370	1371	1372	1373	1374	1375	1376	1377	1378	1379	1380	1381	1382	1383	1384	1385	1386	1387	1388	1389	1390	1391	1392	1393	1394	1395	1396	1397	1398	1399	1400	1401	1402	1403	1404	1405	1406	1407	1408	1409	1410	1411	1412	1413	1414	1415	1416	1417	1418	1419	1420	1421	1422	1423	1424	1425	1426	1427	1428	1429	1430	1431	1432	1433	1434	1435	1436	1437	1438	1439	1440	1441	1442	1443	1444	1445	1446	1447	1448	1449	1450	1451	1452	1453	1454	1455	1456	1457	1458	1459	1460	1461	1462	1463	1464	1465	1466	1467	1468	1469	1470	1471	1472	1473	1474	1475	1476	1477	1478	1479	1480	1481	1482	1483	1484	1485	1486	1487	1488	1489	1490	1491	1492	149

FIG. 27 C



7872-020 (SHEET 31 OF 63)

RSV	Papilio	AVG. IC60 (XIT) ug/m
T-12		
T-13		
T-15		
T-19		
T-28		
T-29		
T-30		
T-69		
T-70		
T-66		
T-576		

Fig. 27D







7872-020 (SHEET 33 OF 63)

RSV	Peptide #	AVG. IC50 [XTT] ug/ml
T-71	P I I I N F Y O P L V F P S D E F D A S I S Q V N E K I N Q S L A F I R	138
T-344	R M K O L E D K V E E L L S K I L A F I R K S D E L L M N V	NOT TESTED
T-613	DELLHNNVNAOKST	>100
T-614	K S D E L L H N V N A O K S T	>100
T-615	I R K S D E L L H M V N A O K S T	>100
T-616	A F I R K S D E L L H M V N A O K S T	>100
T-617	F D A S I S Q V N E K I N Q S L A F I	NOT TESTED
T-682	S L A F I R K S D E L L H N V N A O K S T	>100
T-683	F D A S I S Q V N E K I N Q S L A F I R K	NOT TESTED
T-685	F D A S I S Q V N E K I N Q S L A F I R K S D E L L H N V N A O K	7
T-686	F D A S I S Q V N E K I N Q S L A F I R K S D E L L H N V N A	4
T-687	F D A S I S Q V N E K I N Q S L A F I R K S D E L L H N V	4
T-688	F D A S I S Q V N E K I N Q S L A F I R K S D E L L H	5
T-689	F D A S I S Q V N E K I N Q S L A F I R K S D E L L	80
T-670	F D A S I S Q V N E K I N Q S L A F I R K S D	>100
T-671	A S I S Q V N E K I N Q S L A F I R K S D E L L H N V N A O K S T	8
T-672	I S Q V N E K I N Q S L A F I R K S D E L L H N V N A O K S T	6
T-673	Q V N E K I N Q S L A F I R K S D E L L H N V N A O K S T	14
T-674	H E K I N Q S L A F I R K S D E L L H N V N A O K S T	>100
T-675	K I N Q S L A F I R K S D E L L H N V N A O K S T	>100
T-676	N Q S L A F I R K S D E L L H N V N A O K S T	>100
T-730	F D A S I S Q V N E K I N Q S L A F I R K S D E L L H N V N A O K S T	NOT TESTED

FIG. 28B







7872-020 (SHEET 35 OF 63)

HPV-3 DP107-Like Waits		AVG. IC50	
T-42	A T S A Q I T A A V A L V E A K Q A R S D I E K L K E A I R D T N K A	843,000 ug/hr	
T-43	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A	853,000 ug/hr	
T-38	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	770,000 ug/hr	
T-38	A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	700,000 ug/hr	
T-40	A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S I O N L I V A	58,758 ug/hr	
T-44	A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S I O N L I V A	225,140 ug/hr	
T-45	A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S I O N L I V A	488,000 ug/hr	
T-46	A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S I O N L I V A	648,000 ug/hr	
T-52	L K E A I R D T N K A V Q S S I O N L I V A I K S	137,854 ug/hr	

29B







7872-020 (SHEET 37 OF 63)

[illegible]

FIF. 30 B



## 7872-020 (SHEET 38 OF 63)

Fusion ♥ALLMOTI5♥  
Peptide ♣107x178x4♣  
.....RNKRGVFLGFLGFLATAGSAMGAAS ♣♥ XXXXAQSRTLLAGIVQQQQQ

LLDVVKROQELLRLTVWGTKNLQTRVTAIEKYLKDQAQL♣NAWG♥ CAF

♥ALLMOTI5♥  
\*LVS Predicted Coiled -Coil  
RQVCHTTVPWPNASLTPDW \*NND ♥TWQEWERKVDFFLEENITALLEEAIQQ

♣107x178x4♣  
EKNMY ♣ELOKLNSWD\* VF♥ GNXXXXXXXXXXXXXXXXXXXXXXXXXXXXX♣

IYIVMLAKLRQGYRPVFSSPPSYFQXTHTQQDPALPTREGKEGDGGEGGNSSWP

WQIEYIHF

FIG. 31



## 7872-020 (SHEET 39 OF 63)

MTRRRVLSVVVLLAALACRLGAQTPEQPAPPATTVQPTATRQQTSPFRVCELSSHGDLFRFSSD

♠107x178x4♠

IQCPSTGTRENHTEGLLMVFKDNIIPYSF ♠KVRSYTKIVTNLIYNGWYADSVINRHE♠

EKFSVDSY ETDQMDTIYQ CYNVVKMTKD GLTRVYVDRD GVNITVNLKP TGGLANGVRR

YASQTELYDA PGWLIWTYRT RTTVNCLITD MMAKSNSPFD FFVTTTGQTV EMSPFYDGKN

KETFHERADS FHVRTNYKIV DYDNRGTNPQ GERRAFLDKG TYTLWKLEN RTAYCPLQHW

QTFDSTIATE TGKSIHFVTD EGTSSFVTNT TVGIELPDAF KCIEEQVNKT HEKYEAVQD

RYTKGQEAIT YFITSGGLLL AWLPLTPRSL ATVKNLTELT TPTSSPPSSP SPPAPSAARG

STPAAVLRRR RRDAGNATTP VPPTAPGKSL GTLNNPATVQ IQFAYDSLRR QINRMLGDLA

RAWCLEQKRQ NMVLRELTKI NPTTVMSSY GKAVAAKRLG DVISVSQCVP VNQATVTLRK

SMRVPGSETM CYSRPLVSFS FINDTKTYEG QLGTDNEIFL TTKMTEVCQA TSQYYFQSGN

♠107x178x4♠

EIHVYNDYHH FKTIELDGIA TLQTFISLNT ♠SLIENIDFASLELYSRDEQRASNVFD ♠LE♠

\*LVS Predicted Coiled Coil\*

TM Potential

GIFREYNFQAQNIAGLRKDLDNAVSN\* GRNQ FVDGLGELMDSLGSVG QSITN

♠P12LZIPC♠

TM Potential

TM Potential

LVSTVGGLFSSLVSGFISF FK N ♠PFGGMLILVLVAGVVILVISL♠ TRRTRQMS

QQPVQMLYPG IDELAQQHAS GEGPGINPIS KTELQAIMLA LHEQNQEQR AAQRAAGPSV

ASRALQAARDRFPGLRRRRY HDPETAAALL GEAETEF

FIG. 32



7872-020 (SHEET 40 OF 63)

MMDPNSTSED VKFTPDYQV PFVQAFDQAT RVYQDLGGPS QAPLPCVLWP VLPEPLPQQQ

LTAYHVSTAP TGSWFSAPQP APENAYQAYA APQLFPVSDI TQNQQTNQAG GEAPQPGDNS

TVQTAAAVVF ACPGANQGQQ LADIGVPQPA PVAAPARRTR KPQQPESLEE CDSELEI

@DNA Binding@

▲107x178x4▲

+Dimerization+

@KRY KNRVASRKCRK ▲FK@ Q

+LLOHYREVAAAKSSENDRLRLLLKQ▲

MCPSLDVD+ SI IPRTPDVLHE DLLNF

FIG. 33



## 7872-020 (SHEET 41 OF 63)

Fusion

Peptide

♥ALLMOTI5♥

\*LVS Coiled-Coil\*

FAG

♥VVLAGAALGVATAAQITAGIALHQSMLENSQAIDNLRASLETTN

QAIEAIROAGQEMI\*LAVQGVQDYNN♥ ELIPSMNQLSCDLIGQKLGLKLLRYTT

♣P23LZIPC♣

♣P6,12LZIPC♣

♣107x178x4♣

♥ALLMOTI5♥

EILSLFGPSLRD ♣PISA ♣♥EISIQALSYALGGDINKV♣ LEKLGYSGGDL♣

♣P1,12LZIPC♣

LGILES♣ RGIKARI♥ THVDTESYFIVLSIAÿ ♣PTLSEIKGVTVHRLEGV♣ SY

NIGSQEWYTTVPKYVATQGYLISNFDDESSCTFMPEGTVCSQNALYPMSPLLQECL

RGSTKSCARTLVSGSFGNRFILSQGNLIANCASILCKCYTTGTINQDPDKILTYIAA

♣P23LZIPC♣

♣P12LZIPC♣

♥ALLMOTI5♥

\*LVS Coiled-Coil\*

DHCPVVEVNGVTIQVGSRRYPDAVYLHRIDLGP ♣P ♥IS\*LERLDVGTNLGN

♦Transmembrane Region♦

AIAKLEDAKELL♣ ESSDOI\*L♣ RSMK ♦GLSSTSIVYILI♥ AVCLGGLIGIPALICCC♦ RGRCNKKGEQVGMSRPGLKPDLTGTSKSYVRSL

FIG. 34



## 7872-020 (SHEET 42 OF 63)

## Pre S1 and Pre S2

MGQNLSTSNPLGFFPDHQLDPAFRANTANPDWDFNPKNKDTWPDANKVGAGAFG  
LGFTPPHGGLLGWSPQAQGILQTLPANPPPASTNRQSGRQPTPLSPPLRNTHPQAM  
QWNSTTFHQTLQDPRVRGLYFPAGGSSSGTVNPVLTTASPLSSIFSRIGDPALN

## Major Surface Antigen (HBs)

Fusion

Peptide

✦P12 &amp; 23LZIPC✦

MENITSG FLG ✦PLL VLQAGFLLTRLTI✦ PQSLDSWWTSLNFLGGTTVCLG

✦P12 &amp; 23LZIPC✦

QNSQSPTSNHSPTSCPPTC ✦PGYRWMCLRRFIHFLFILLCLIFLLVLLDYQGML✦

PVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPISSWAFGKF

♦Transmembrane Region♦LWEWASARFSWLS ♦LLVPEVQWEVGLSPTVWLSVI♦ WMMWYWGPSL♦Transmembrane Region♦♦YSILSPELPLLPIEFCLWVYI♦

FIG. 35



7872-020 (SHEET 43 OF 63)

Fusion      ♥ALLMOTIS♥      ♠107x178x4♠  
Peptide      \*LVS Coiled Coil  
AIQLIPLFVG LGI ♥TTAVSTGAAGLGVS ♠IT \*QYTKLSHQLISDV

QAISSTIODLODOVDSLAEVVLO\* NRRGLDLLTAE♠ QGGI♥

CLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNPFWTSFHG

FLPYVMPLLGPLLCLLVLSFGPIIFNKLMTFIKHQIESIQAKPIQVHYH

Transmembrane Region

RLEQEDSGGSYLTLT.....????????????????????????????????.....

FIG 36



7872-020 (SHEET 44 OF 63)

MKAQKGFTLI ELMIVVAIIG ILAAIAIPQ

♠107x178x4♠

♥ALLMOTIS♥

♠♥YODYTARTQVTRAYSEVSALKTAAESAILEGKEIVSSA♠ T♥

PK DTQYDIGFT

♠107x178x4♠

♥ALLMOTIS♥

♠♥ESTLLDGSGKSQIQVTDNODGTVELVATLGKSSGS♠ AIKGAVITVSR♥

KNDGV WNCKITKTPT AWKPNYAPAN CPKS

FIG. 37



7872-020 (SHEET 45 OF 63)

MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV

SEAILLAEGQ KSAVTEYYLN HGIWP

♠107x178x4♠

♥ALLMOTI5♥

♠♥KDNTSAGVASSSSIKGKYVKEVKVENGVVTTAT♠

MNSSNVNKEIQGKKLSLWAKRQDGSVKW♥

FCGQP VTRNAKDDTV TADATGNDGK IDTKHLPSTC RDNFDAS

FIG. 38



7872-020 (SHEET 46 OF 63)

MKKTLLGSLI LLAFAAGNVQA DINTETSGKV TFFGKVVENT

CKVKTEHKNL SVVLNDVGKN SLSTKVNTAM PTPFTITLQN

CDPTTANGTA NKANKVGLYF Y

♠107x178x4♠

♥ALLMOTIS♥

♠♥SWKNVDKENNETLKNEOTTADYATNVNI♠

QLMESNGTKAISVVGKETE♥

DF MHTNNGVAL NQTHPNNAHI SGSTQLTTGT NELPLHFIAQ

YYATNKATAG KVVQSSVDFQI AYE

FIG. 39



## 7872-020 (SHEET 47 OF 63)

MNKKLLMNFF IVSPLLATT ATDFTPVP

♠107x178x4♠

♥ALLMOTIS♥

♠♥LSSNQIIKTAKASTNDNIKDLLDWYSSGSDTETNS♠♥

EVLDNSL GSMRIKNTDG SISLIIFPSP YYSFAFTKGE KV

♠107x178x4♠

♠DLNTRKRTKKSQHTSEGTYIHFQISGVT♠

N TEKLPTIEL PLKVKVHGKD SPLKYG

♣P12LZIPC♣

♣PKFDKKQLAISTLDFEIRHQLTQI♣

HGLYRSSDKT GGYWKITMND GSTYQSDLSK KFEYNTEKPP

INIDEIKTIE AEIN

FIG. 40



7872-020 (SHEET 48 OF 63)

♥ALLMOTIS♥  
MKKTAFILL FIALTLTTSP L ♥VNG

♠107x178x4♠  
\*LVS Predicted Coiled-Coil\*  
\*S ♠EKSEEINEKDLRKKSELORNALSNLROIY\* YNEKAITENKESDD♠

QFLENTLL♥FKGFFTGHWP

♠107x178x4♠  
♠YNDLLVDLGSKDATNKYKGKKVDLYGAY♠

YGYQCAGGTPNKTACMYGGVTLHDN NRLTEKKVP INLWIDGKQTTV

♣P12LZIPC♣  
♣PIDKVKTSKKEVTQELDL♣ QARHYLHGK FGLYNSDSFGGKVQ

♣P12LZIPC♣  
RGLIVF HSSEGSTVSY DLFDAQGQY ♣P DTLRIYRDN KTINSENLHI♣

DLYLYTT

FIG. 41



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MKKTAFTLLL FLALTLTTSP L ♡ALLMOTIS♡  
♡VNGS

♠107x178x4♠

♠EKSEEINEKDLRKKSELOGTALGNLKOIYYNEKAKTENKESHDA ♠ Q♡

FLQHTILFKG FFTDHSWYND LLVDFDSKDI VDKYKGKKVDLYGAYY

GYQC AGGTPNKTAC MYGGVTLHDN NRLTEKKVPINLWLDGKQNTV

♠107x178x4♠

♡ALLMOTIS♡

♣P12LZIPC♣

♣P ♡L ♠ETVKTNNKNVTVOELDLOARRYLA ♠ QEKYNLYN♠

SDVFDGKVQR♡ GLIVF HTSTE

♣P23LZIPC♣

♣PSVNYDLFGAQQQYSNTLLRIYRDNKTINSENMI♣ DIYLYTS

FIG. 42



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MKNITFIFILLASPLYANGDRLYRADSRPPDEIKRFRSLMPRGNEYFDRGT

♥ALLMOTI5♥

♥QMNINLYDHARGTQTGFVRYDDGYV

♠107x178x4♠

♠STSLSLRSAHLA GOYILSGYSLTIYIVI♠ ANMFNVNDVISVY♥

SP HPYEQEVSAL GGIPYSQIYG WYRVNFGVID ERLHRNREYR

DRYYRNLNIA PAEDGYRLAG FPPDHQAWRE EPWIHHAPQG

CGDSSRTITG DTCNE

♥ALLMOTI5♥

♥ETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL♥

FIG. 43



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MMFSGFNADY EASSSRCSSA SPAGDSLSYY HSPADSFSSM

GSPVNAQDFC TDLAVSSANF IPTVTAISTS PDLQWLQPA

LVSSVAPSQT RAPHPFGVPA PSAGAYSRAG VVKMTGGRA

\*LVS Predicted Coiled-Coil\*

QSIGRRGKVE QLSPEEEER RIRRE \*RNKMA AAK

♠107x178x4♠

♥ALLMOTIS♥

♥CRNRRREL ♠TDTLQAETDOLEDEKSALOTEIANLLKEKEKL♥

EFILAAH R\* PACKIPDDL GFPEEMSVAS LDLTGGLPEV

ATPESEEAFT LPLLNDPEPK PSVEPVKSIS SMELKTEPFD

DFLFPASSRP SGSETARSVP DMDLSGSFYA LPLLNDPEPK

PSVEPVKSIS SMELKTEPFD DFLFPASSRP SGSETARSVP

DMDLSGSFYA GSSSNEPSSD SLSSPTLLAL

FIG. 44



## 7872-020 (SHEET 52 OF 63)

SGWESYYKTEGDDEEAEEEQEENLEASGDYKYSGRDSLIFLVDASKA  
 MFESQSEDELTPFDMSIQCIQSVYISKIISDRDLLAVVFGTEKDKNS  
 VNFKNITYVLQELDNPGAKRILELDQFKGQQGQKRFQDMMGHGSDY  
 SLSEVLWVCANLFSDVQFKMSHKRIMLFTNEDNPHGNDSAKASRAR  
 TKAGDLRDTGIFLDMHLKKPGGFDISLFYRDIISIAEDED

♠107x178x4♠

♥ALLMOTIS♥

\*LVS Predicted Coiled-Coil\*

♥LRVH \*FEE ♠SSKLEDLLRKVRAKETRKRALSRLKLKLNKDIV\* ISV

GIYNLVQKAL♥ KPPPIKLYRETN♠ EPVKTkTRTFNTSTGGLLLPSDTKR

SQIYGSRQIILEKEETEELKRFDGPGLMLMGFKPLVLLKKHHLRPSLFVYPE  
 ESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQK  
 IQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIVEKLRFTYRS  
 DSFENPVLQQHFRNLEALALDLME

♠P12LZIPC♠

♠PEQAVDLTLPKVEAMNKRL♠ GSLVDEFKELVYPPDYNPEGKVTKR

KHDNEGSGSKRPKVEYSEEELKTHISKGTLGKFTVPMLKEACRAYGLKSG

LKKQELLEALTKHFQD

FIG. 45



7872-020 (SHEET 53 OF 63)

GGGALSPQHSAVTQGSIIKNKEGMDAKS

♠107x178x4♠

♥ALLMOTIS♥

♥♠LTAWSRTLVTFKDVFVDETREEWKLLDT♠ AQQIVYRNV

MLENYKNLVSLGYQLT♥ KPDVILRLEKGEEPWLVEREIHQETHPD  
SETAFEIKSSVSSRSIFKDKQSCDIKMEGMARNDLWYLSLEE VWKCR  
DQLDKYQENPERHLRHQLIHTGEKPYECKECKGKSFSRSSHLIGHQKT  
HTGEEPYECKECKGKSFSWFSHLVTHQRTHTGDKLYTCNQCGKSFVH  
SSRLIRHQRTHTGHKPYECPECKGKSFRQSTHLILHQRTHVVRVPYECN  
ECGKSYSQRSHLVVHHRIHTGLKPFECKDCGKCFSSRSHLYSHQRT  
TGEKPYECHDCGKSFSQSSALIVHQRIHTGEKPYECCQCGKAFIRKN  
DLIKHQRIHVGAETYKCNQCGIIFSQNS

♣P23LZIPC♣

♣PFIVHQIAHTGEQFLTCNQCGTALVNTSNLIGYQTNHI♣ RENAY

FIG. 46











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HIV-1 BRU Walks N-Terminal to DP178									
AA1	AA2	AA3	AA4	AA5	AA6	AA7	AA8	AA9	AA10
1	2	3	4	5	6	7	8	9	10
11	12	13	14	15	16	17	18	19	20
21	22	23	24	25	26	27	28	29	30
31	32	33	34	35	36	37	38	39	40
41	42	43	44	45	46	47	48	49	50
51	52	53	54	55	56	57	58	59	60
61	62	63	64	65	66	67	68	69	70
71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90
91	92	93	94	95	96	97	98	99	100
101	102	103	104	105	106	107	108	109	110
111	112	113	114	115	116	117	118	119	120
121	122	123	124	125	126	127	128	129	130
131	132	133	134	135	136	137	138	139	140
141	142	143	144	145	146	147	148	149	150
151	152	153	154	155	156	157	158	159	160
161	162	163	164	165	166	167	168	169	170
171	172	173	174	175	176	177	178	179	180
181	182	183	184	185	186	187	188	189	190
191	192	193	194	195	196	197	198	199	200
201	202	203	204	205	206	207	208	209	210
211	212	213	214	215	216	217	218	219	220
221	222	223	224	225	226	227	228	229	230
231	232	233	234	235	236	237	238	239	240
241	242	243	244	245	246	247	248	249	250
251	252	253	254	255	256	257	258	259	260
261	262	263	264	265	266	267	268	269	270
271	272	273	274	275	276	277	278	279	280
281	282	283	284	285	286	287	288	289	290
291	292	293	294	295	296	297	298	299	300
301	302	303	304	305	306	307	308	309	310
311	312	313	314	315	316	317	318	319	320
321	322	323	324	325	326	327	328	329	330
331	332	333	334	335	336	337	338	339	340
341	342	343	344	345	346	347	348	349	350
351	352	353	354	355	356	357	358	359	360
361	362	363	364	365	366	367	368	369	370
371	372	373	374	375	376	377	378	379	380
381	382	383	384	385	386	387	388	389	390
391	392	393	394	395	396	397	398	399	400
401	402	403	404	405	406	407	408	409	410
411	412	413	414	415	416	417	418	419	420
421	422	423	424	425	426	427	428	429	430
431	432	433	434	435	436	437	438	439	440
441	442	443	444	445	446	447	448	449	450
451	452	453	454	455	456	457	458	459	460
461	462	463	464	465	466	467	468	469	470
471	472	473	474	475	476	477	478	479	480
481	482	483	484	485	486	487	488	489	490
491	492	493	494	495	496	497	498	499	500
501	502	503	504	505	506	507	508	509	510
511	512	513	514	515	516	517	518	519	520
521	522	523	524	525	526	527	528	529	530
531	532	533	534	535	536	537	538	539	540
541	542	543	544	545	546	547	548	549	550
551	552	553	554	555	556	557	558	559	560
561	562	563	564	565	566	567	568	569	570
571	572	573	574	575	576	577	578	579	580
581	582	583	584	585	586	587	588	589	590
591	592	593	594	595	596	597	598	599	600
601	602	603	604	605	606	607	608	609	610
611	612	613	614	615	616	617	618	619	620
621	622	623	624	625	626	627	628	629	630
631	632	633	634	635	636	637	638	639	640
641	642	643	644	645	646	647	648	649	650
651	652	653	654	655	656	657	658	659	660
661	662	663	664	665	666	667	668	669	670
671	672	673	674	675	676	677	678	679	680
681	682	683	684	685	686	687	688	689	690
691	692	693	694	695	696	697	698	699	700
701	702	703	704	705	706	707	708	709	710
711	712	713	714	715	716	717	718	719	720
721	722	723	724	725	726	727	728	729	730
731	732	733	734	735	736	737	738	739	740
741	742	743	744	745	746	747	748	749	750
751	752	753	754	755	756	757	758	759	760
761	762	763	764	765	766	767	768	769	770
771	772	773	774	775	776	777	778	779	780
781	782	783	784	785	786	787	788	789	790
791	792	793	794	795	796	797	798	799	800
801	802	803	804	805	806	807	808	809	810
811	812	813	814	815	816	817	818	819	820
821	822	823	824	825	826	827	828	829	830
831	832	833	834	835	836	837	838	839	840
841	842	843	844	845	846	847	848	849	850
851	852	853	854	855	856	857	858	859	860
861	862	863	864	865	866	867	868	869	870
871	872	873	874	875	876	877	878	879	880
881	882	883	884	885	886	887	888	889	890
891	892	893	894	895	896	897	898	899	900
901	902	903	904	905	906	907	908	909	910
911	912	913	914	915	916	917	918	919	920
921	922	923	924	925	926	927	928	929	930
931	932	933	934	935	936	937	938	939	940
941	942	943	944	945	946	947	948	949	950
951	952	953	954	955	956	957	958	959	960
961	962	963	964	965	966	967	968	969	970
971	972	973	974	975	976	977	978	979	980
981	982	983	984	985	986	987	988	989	990
991	992	993	994	995	996	997	998	999	1000

FIG. 49A



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[illegible]

F. 16. 49B



7872-020 (SHEET 58 OF 63)

[illegible]

F-16 49C







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Residue	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000	1001	1002	1003	1004	1005	1006	1007	1008	1009	1010	1011	1012	1013	1014	1015	1016	1017	1018	1019	1020	1021	1022	1023	1024	1025	1026	1027	1028	1029	1030	1031	1032	1033	1034	1035	1036	1037	1038	1039	1040	1041	1042	1043	1044	1045	1046	1047	1048	1049	1050	1051	1052	1053	1054	1055	1056	1057	1058	1059	1060	1061	1062	1063	1064	1065	1066	1067	1068	1069	1070	1071	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090	1091	1092	1093	1094	1095	1096	1097	1098	1099	1100	1101	1102	1103	1104	1105	1106	1107	1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	1119	1120	1121	1122	1123	1124	1125	1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148	1149	1150	1151	1152	1153	1154	1155	1156	1157	1158	1159	1160	1161	1162	1163	1164	1165	1166	1167	1168	1169	1170	1171	1172	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1185	1186	1187	1188	1189	1190	1191	1192	1193	1194	1195	1196	1197	1198	1199	1200	1201	1202	1203	1204	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227	1228	1229	1230	1231	1232	1233	1234	1235	1236	1237	1238	1239	1240	1241	1242	1243	1244	1245	1246	1247	1248	1249	1250	1251	1252	1253	1254	1255	1256	1257	1258	1259	1260	1261	1262	1263	1264	1265	1266	1267	1268	1269	1270	1271	1272	1273	1274	1275	1276	1277	1278	1279	1280	1281	1282	1283	1284	1285	1286	1287	1288	1289	1290	1291	1292	1293	1294	1295	1296	1297	1298	1299	1300	1301	1302	1303	1304	1305	1306	1307	1308	1309	1310	1311	1312	1313	1314	1315	1316	1317	1318	1319	1320	1321	1322	1323	1324	1325	1326	1327	1328	1329	1330	1331	1332	1333	1334	1335	1336	1337	1338	1339	1340	1341	1342	1343	1344	1345	1346	1347	1348	1349	1350	1351	1352	1353	1354	1355	1356	1357	1358	1359	1360	1361	1362	1363	1364	1365	1366	1367	1368	1369	1370	1371	1372	1373	1374	1375	1376	1377	1378	1379	1380	1381	1382	1383	1384	1385	1386	1387	1388	1389	1390	1391	1392	1393	1394	1395	1396	1397	1398	1399	1400	1401	1402	1403	1404	1405	1406	1407	1408	1409	1410	1411	1412	1413	1414	1415	1416	1417	1418	1419	1420	1421	1422	1423	1424	1425	1426	1427	1428	1429	1430	1431	1432	1433	1434	1435	1436	1437	1438	1439	1440	1441	1442	1443	1444	1445	1446	1447	1448	1449	1450	1451	1452	1453	1454	1455	1456	1457	1458	1459	1460	1461	1462	1463	1464	1465	1466	1467	1468	1469	1470	1471	1472	1473	1474	1475	1476	1477	1478	1479	1480	1481	1482	1483	1484	1485	1486	1487	1488	1489	1490	1491	1492	1493	1494	1495	1496	1497	1498	1499	1500	1501	1502	1503	1504	1505	1506	1507	1508	1509	1510	1511	1512	1513	1514	1515	1516	1517	1518	1519	1520	1521	1522	1523	1524	1525	1526	1527	1528	1529	1530	1531	1532	1533	1534	1535	1536	1537	1538	1539	1540	1541	1542	1543	1544	1545	1546	1547	1548	1549	1550	1551	1552	1553	1554	1555	1556	1557	1558	1559	1560	1561	1562	1563	1564	1565	1566	1567	1568	1569	1570	1571	1572	1573	1574	1575	1576	1577	1578	1579	1580	1581	1582	1583	1584	1585	1586	1587	1588	1589	1590	1591	1592	1593	1594	1595	1596	1597	1598	1599	1600	1601	1602	1603	1604	1605	1606	1607	1608	1609	1610	1611	1612	1613	1614	1615	1616	1617	1618	1619
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FIG. 51B



## 7872-020 (SHEET 62 OF 63)

## Domain I:

174P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-S-P220

P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T  
L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T  
L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V  
V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C  
L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L  
Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G  
A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q  
G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N  
F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S  
F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q  
L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-S

F=Ig, 52A







## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US95/16733

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) : C07K 7/04, 14/025, 14/16; C12N 9/94, 9/96, 9/98, 9/99

US CL : 530/324; 424/184.1

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/324, 325, 326, 327, 328, 329; 424/184.1, 185.1, 186.1, 187.1, 188.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MEDLINE, AIDSLINE, APS

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ----- Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 89, Number 21, issued November 1992, Wild et al, "A Synthetic Peptide Inhibitor of Human Immunodeficiency Virus Replication: Correlation Between Solution Structure and Viral Inhibition", pages 10537-41, see entire document.	1-3, 9, and 10 ----- 4-8 and 11-15

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	
* A	document defining the general state of the art which is not considered to be of particular relevance		
* E	earlier document published on or after the international filing date	X	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
* L	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	Y	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
* O	document referring to an oral disclosure, use, exhibition or other means		
* P	document published prior to the international filing date but later than the priority date claimed	A	document member of the same patent family

Date of the actual completion of the international search

28 MARCH 1996

Date of mailing of the international search report

09 APR 1996

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
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Washington, D.C. 20231

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Telephone No. (703) 308-0196



## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US95/16733

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ----- Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 91, Number 26, issued December 1994, Wild et al, "Propensity for a Leucine Zipper-Like Domain of Human Immunodeficiency Virus Type 1 gp41 to Form Oligomers Correlates With a Role in Virus-Induced Fusion Rather Than Assembly of the Glycoprotein Complex", pages 12676-80, see entire document.	1-3, 9 and 10 ----- 4-8 and 11-15
X ----- Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 81, Number 24, issued December 1984, Collins et al, "Nucleotide Sequence of the Gene Encoding the Fusion (F) Glycoprotein of Human Respiratory Syncytial Virus", pages 7683-87, see pages 7683 and 7685.	1 and 4 ----- 9 and 11
X ----- Y	VIROLOGY, Volume 204, Number 2, issued 01 November 1994, Bousse et al, "Regions on the Hemagglutinin-Neuraminidase Proteins of Human Parainfluenza Virus Type-1 and Sendai Virus Important for Membrane Fusion", pages 506-514, see pages 506 and 510-513.	1 and 5 ----- 9 and 12
X ----- Y	JOURNAL OF VIROLOGY, Volume 67, Number 9, issued September 1993, Wang et al, "Ion Channel Activity of Influenza A Virus M2 Protein: Characterization of the Amantidine Block", pages 5585-94, see pages 5585-86.	1 and 6 ----- 9 and 13
X ----- Y	JOURNAL OF VIROLOGY, Volume 67, Number 5, issued May 1993, Lazinski et al, "Relating Structure to Function in the Hepatitis Delta Virus Antigen", pages 2672-80, see pages 2672-73 and 2678.	1 and 7 ----- 9 and 14
P, Y	JOURNAL OF EXPERIMENTAL MEDICINE, Volume 182, Number 2, issued August 1995, Suzuki et al, "Viral Interleukin 10 (IL-10), the Human Herpes Virus 4 Cellular IL-10 Homologue, Induces Local Anergy to Allogenic and Syngeneic Tumors", pages 477-486, see entire document.	1, 8, 9, and 15



